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					Table 8		
6046	Table 3A	Hs.146381	BE613237	9894834	RNA binding motif protein, X chromosome (RBMX), mRNA	-1	ACTGACCTAGCAGATGTGTGGAAAAG GAATCAGATCTTGATTCTTCTGGG
6047	Table 3A	Hs.4310	BE614297	9895894	/cds=(11,1186) eukaryotic translation initiation factor 1A (EIF1A), mRNA /cds=(207,641)	-1	ACAACTCAAGTGAAAAGATGTCTCCA GTTTCTGAAGATAACGCACGCTGA
6048	Table 3A	Hs.198802	BE621611	9892551	601493754T1 cDNA, 3' end /clone=IMAGE:3895836 /clone_end=3'	-1	CGCCGACTCGTTGAAAGTTTTGTTGT GTAGTTGGTTTTCGTTGAGTTCTT
6049	Table 3A	Hs.324481	BE646433	9970744	EST380617 cDNA	-1	CACCCACCTGGTAGGAAGGTCAATCT TATGCTCAGAAGTCCCACCCACCA
6050	db mining	Hs.283165	BE646441	9970752	7e86h06.x1 cDNA, 3' end /clone=IMAGE:3292091 /clone_end=3'	-1	CAACTCCTTAAAGGGTTGAAGGTTGT GACAATAACTGAGGGAACTGATGT
6051	Table 3A	Hs.341573	BE646470	9970781	tc38c11.x1 cDNA, 3' end /clone=IMAGE:2066900 /clone_end=3'	-1	AAAACACTCCACCTAAAAGCAGGAAA GATGGCAATTCTAAATAGCAGCTA
6052	db mining	Hs.283166	BE646492	9970803	7e87g01.x1 cDNA, 3' end /clone=IMAGE:3292176 /clone_end=3'	-1	GGAGGTTTTGATCGTGACTTTATTTT GAGATATTGTATCTTTGTTAGTATTGC
6053	Table 3A	Hs.187872	BE646499	9970810	7e87h02_x1 cDNA, 3' end /clone=IMAGE:3292179 /clone_end=3'	-1	TTGTAAGGTTCCGGGGAACTGACTCA ACATGGTTCTCCAACTCGAGGTTG
6054	db mining	Hs.283167	BE646510	9970821	7e88b08.x1 cDNA, 3' end /clone=IMAGE:3292215 /clone_end=3'	-1	TGTGAGTGTTATAGGTTACAGTGGAT TCCAAACTAGCCACAAGTGAAGCA
6055	db mining	Hs.283168	BE646569	9970860	7e89c01.x1 cDNA, 3' end /clone=IMAGE:3292320 /clone_end=3'	-1	TCAGCCAGGAGGAAAAGCACTCTGAT TATGAATTGAGCAGAAAGGAAACAA
8058	db mining	Hs.283169	BE646617	9970926	7e91b07.x1 cDNA, 3' end /clone=IMAGE:3292501 /clone_end=3'	-1	GTTCCCACTCGTTCTTGCCGGAGAAA CCTGCCTTTTCAAGCATAATTCAA
6057	db mining	Hs.225200	BE646640	9970951	7e91f08.x1 cDNA, 3' end /clone=IMAGE:3292551 /clone_end=3'	-1	GGGTCCAAGATTATTGATTAATTTGG GCACCGCGAGAGCTCGAGTCCCCC
6058	Table 3A	Hs.129192	BE670564	10031125	7e36h08.x1 cDNA, 3' end /clone=IMAGE:3284607 /clone_end=3'	-1	GACCACCTGTAAAGCAAGTCCTTTCA AGTTTCACTGCACATCCCAAACCA
6059	Table 3A	Hs.75703	BE670604	10031345	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(106,386)	-1	TGGTCCACTGTCACTGTTTCTCTGCT GTTGCAAATACATGGATAACACAT
6080	Table 3A	Hs.195374	BE671615	10032445	7a47c12.x1 cDNA, 3' end /clone=IMAGE:3221676 /clone_end=3'	-1	AGACTCTGGAAAAGGAGGGTCGGAG TATTAAACTGGCTGGGAATGAGAGG
6061	Table 3A	NA	· BE672733	10033274	7b75g07.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:3234108 3' similar to TR:O99231 O99231 CYTOCHROME OXIDASE	-1	TGAGAGCACACCATAAATTCACAGCA GGAATAAACGAAGACACACGAGCA
6062	Table 3A	Hs.77542	BE873364	10033905	602629438F1 cDNA, 5' end /clone=IMAGE:4754432 /clone_end=5'	-1	ACATTCTCTCATTTTGCTGAAGCTGAT TTGATTGGGTGTCTGTTTCTCGC
6063	Table 3A	Hs.86357	BE673759	10034300	7d69d02.x1 cDNA, 3' end /clone=IMAGE:3278211 /clone_end=3'	-1	TGAGAAGGTAAAGTAGAAAGGGAAG ATGATGAGTGAACAATAAGCCTTGT
6064	db mining	Hs.283246	BE674662	10035284	7e93g03.x1 cDNA, 3' end /clone=IMAGE:3292756 /clone_end=3'	-1	ACATTATTCCATGGGAATAAGTCATC AGTGCAAAGGACTGTAAGGAGTGC
6065	Table 3A	Hs.88845	BE674685	10035307	AV733781 cDNA, 5' end /clone=cdAASF08 /clone_end=5'	-1	CGCCGCTCCTGGAGACCTGATAACTT AGGCTTGAAATAATTGACTTGTCT
6066	Table 3A	Hs.171120	BE674709	10035331	7e94f05.x1 cDNA, 3' end /clone=IMAGE:3292833 /clone_end=3'	-1	TGTATGTGCAATATGCTTATGGGTAA TTATGGGCAAGAGAAATGGAAACA
6067	db mining	Hs.283249	BE674713	10035335	7e94g02.x1 cDNA, 3' end /clone=IMAGE:3292850 /clone_end=3'	-1	ACCCCTTGGTAAAGCAGTTGTAAGAA TTAAACAAGAGGAATTGCTCTTTC
6068	Table 3A	Hs.167208	BE674762	10035230	7e98d05.x1 cDNA, 3' end /clone=IMAGE:3293193 /clone_end=3'	-1	AAATCAGGCCCCTTGCGCCATTCACA AAAATCCTTGTGAGATGACTCAAG
6069	db mining	Hs.283247	BE674807	10035275	7e93d11.x1 cDNA, 3' end /clone=IMAGE:3292725 /clone_end=3'	-1	AGGGCAGAGGTCCTTTGGGAGGGTA AGCTCACAAAAACTCAGGGAGGCAG
6070	Table 3A	Hs.174010	BE674902	10035443	7e97a04.x1 cDNA, 3' end /clone=IMAGE:3293070 /clone_end=3'	-1	TCATCTCCGCCAAGGTTCCCACTAGG CAGGAAAGGATTTTTATCTAAAGT
6071	Table 3A	Hs.174144	BE674951	10035492	7e97g10.x1 cDNA, 3' end /clone=IMAGE:3293154 /clone_end=3'	-1	CCACCCAAGTCGGAATCCGAGTGAA ATAAATAGCATCGCCCGCCAACTAC
6072	Table 3A	Hs.190 0 65	BE674964	10035505	7f11b09.x1 cDNA, 3' end /clone=IMAGE:3294329 /clone_end=3'	-1	AGGCACACGATTGTCACCATTTCTCC CTTTACAAGCTGTATAATCAGTAA
6073	Table 3A	Hs.211828	BE675092	10035633	7f02d07.x1 cDNA, 3' end /clone=IMAGE:3293485 /clone_end=3'	-1	GCAACGTCTGAATGTAGTAATGTGAC TCAGAGCTTCAAAGTAAGCATTCG

					Table 8		
6074	db mining	Hs.330706	BE675125	10035666	IL3-UT0114-301100-357-H02 cDNA	-1	GCCACCCCATCTGGGAGGCCCAGCA TCCAATTCAGTCGCCTTCAATGATT
6075	db mining	Hs.283251	BE675180	10035721	7f03h06.x1 cDNA, 3' end /clone=IMAGE:3293627 /clone_end=3'	-1	TGATAGACTGGATGCTGCTATGGTAA TCTGCCTCAGGAAAATGCCGGACT
6076	db mining	Hs.339261	BE675338	10035879	HNC29-1-D4.R cDNA	-1	TGGAGCCAAGAAGCCACTGACTCAA GAGGATTTCAAGCGAGAGCTGCTTG
6077	db mining	Hs.283253	BE675379	10035920	7f08b02.x1 cDNA, 3' end /clone=IMAGE:3294027 /clone_end=3'	-1	CAACTTTTGTAACAGGGGACTTAGCC GGGGGCAGGAGGGGTTCTTGAGAC
6078	db mining	Hs.283254	BE675403	10035944	7f08d10.x1 cDNA, 3' end /clone=IMAGE:3294067 /clone_end=3'	-1	ACTTGAAGGCACATCTTCCTTTTGGT TGTTTTCCATCTTCAAATTAAACT
6079	dio mining	Hs.283255	BE675434	10035975	7f09a10.x1 cDNA, 3' end /clone=IMAGE:3294138 /clone_end=3'	-1	TAAAAACTGACATGACATGAGATGGT TTAAGTGTCAAACATAAGGGTCTTT
6080	dio mining	Hs.283256	BE675531	10036072	7f10h08.x1 cDNA, 3' end /clone=IMAGE:3294303 /clone_end=3'	-1	ACTGACATAAGCCCACTTCAGGTGTT TGGAAGACACTAAAGAGAATCAGA
6081	db mining	Hs.315345	BE675610	10036151	7f12g09.x1 cDNA, 3' end /done=IMAGE:3294496 /done_end=3'	-1	GCAGCTTTTTGCTGGCGGGGGTCTA AATAAAGTAGCTTCCCCAAAAGAAA
6082	db mining	Hs.180637	BE675718	10036259	7f14h04.x1 cDNA, 3' end /clone=IMAGE:3294679 /clone_end=3'	-1	ACCTGGTTATCTCGCAATGACCTAGC TAACACAAATGCAACATCAGCCGG
6083	db mining	Hs.283258	BE675792	10036333	7f16b02.x1 cDNA, 3' end /clone=IMAGE:3294795 /clone_end=3'	-1	TGATCAAAATGAAGATGCTCCAACCG TATAAATGGCAGATGAAATAGACT
6084	db mining	Hs.283259	BE675819	10036360	7f17d10.x1 cDNA, 3' end /clone=IMAGE:3294931 /clone_end=3'	-1	GCAGGAGAGAAATACCTTCTAATGGG TGTGGACACTGGAGGAACTGTTAC
6085	db mining	Hs.283261	BE675957	10036498	7f19b06.x1 cDNA, 3' end /clone=IMAGE:3295091 /clone_end=3'	-1	AGGGCACTGTTTGTTCCTTTAATATG GAGAAATATCGCAAATAACTGGGA
6088	db mining	NA ·	BE676019	10036560	7f20c12.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:3295222 3' similar to contains Alu repetitive element;, m	-1	TTGGCCTATGTTAATTTCTATTCTCAG TTCTTCTGTGCCCTTCCTCCTCT
6087	Table 3A	Hs.170584	BE676049	10036590	7f21a03.x1 cDNA, 3' end /clone=IMAGE:3295276 /clone_end=3'	-1	GAACGTAAGCCCGACGCTAGGCAGT GCTGTTAGAAAGTGATTTGGAAGAG
6088	Table 3A	Hs.181015	BE676054	10036595	signal transducer and activator of transcription 6, interleukin-4 induced (STAT6), mRNA /cds=(165,2708)	-1	ATCCCATTCTCCCTCTCAAGGCAGGG GTCATAGATCCTAAGCCATAAAAT
6089	db mining	Hs.283263	BE676154	10036695	7f24a12.x1 cDNA, 3' end /clone=IMAGE:3295582 /clone_end=3'	-1	TGCTGTAAAATGGCAGCTCCATAGGA ACCTATTTTCCATAGGAACCTGCA
6090	db mining	Hs.283284	BE676173	10036714	7f24c12.x1 cDNA, 3' end /clone=IMAGE:3295606 /clone_end=3'	-1	ACTGGAGAAAGGTGTCTTCCTGTCCT TTCAGGGGCTCCTGCGGGGAATTC
8091	Table 3A	Hs.134648	BE876210	10036751	7f25c05.x1 cDNA, 3' end /clone=IMAGE:3295688 /clone_end=3'	-1	ATTATATTTGTCCCTATCAGAATCCTC GAATCCCTAGCAGCCAGTCCCTG
6092	db mining	Hs.283266	BE676275	10036816	7f26d04.x1 cDNA, 3' end /clone=IMAGE:3295783 /clone_end=3'	-1	TGCTCACTGTCTTCTGGAAGAGACAA GCACTTTCTTGAAATTCCTAAGCA
6093	Table 3A	Hs.158714	BE876408	10036949	7f29b11.x1 cDNA, 3' end /clone=IMAGE:3296061 /clone_end=3'	-1	CAATCGGATCATTCTTCTCAACTTGG GCGGCTCTTTCCTCCCTTCCTTCC
6094	Table 3A	Hs.220929	BE676472	10037003	cDNA FLJ14369 fis, clone HEMBA1001174, highly similar to ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 5 /cds=(207,746)	-1	TGCTTTGGGCAGTAGCTGAAGCCGA AGTATGAACAGTCCATTTTGTTTCT
6095	db mining	Hs.283268	BE676474	10037005	7f30c08.x1 cDNA, 3' end /clone=IMAGE:3296174 /clone_end=3'	-1	CACAGTTGAGTAGGAGGTCATGAAGA AGAAGAGATGATACCTGCCTTACC
6096	db mining	Hs.283269	BE676528	10037069	7f31d12.x1 cDNA, 3' end /clone=IMAGE:3296279 /clone_end=3'	-1	TTTGTGTAGCAAATGTTCATTAATTGC CTACTTTGTGCCAAATTCAGGCC
6097	Table 3A	Hs.123254	BE676541	10037082	AL572805 cDNA /clone=CS0Dl034YH06-(3-prime)	-1	TCCAGCATTGTATTGTCTATTGACAC ACAAAGTTTGAAAATAAAGGGGCA
6098	d b mining	Hs.283505	BE676548	10037089	wh79f01.x1 cDNA, 3' end /clone=IMAGE:2386969 /clone_end=3'	-1	CACCCACCAGACCGAGGATTCCAAAA GGGGGCGAAGGCGGAGGCAAAGG
6099	db mining	Hs.283270	BE676613	10037154	7f33a08.x1 cDNA, 3' end /clone=IMAGE:3296438 /clone_end=3'	-1	TGGACTCTGTTTTCAAGAGGAAGAAA CAACTGACAAATAAGTTGATGTCA
6100	db mining	Hs.283271	BE676614	10037155	7f33a10.x1 cDNA, 3' end /clone=IMAGE:3296442 /clone_end=3'	-1	ATGTTGAAACTGGTTTTAACTTGTAAT GGTGTGGCTGATGTTACCCGACC
6101	db mining	Hs.283272	BE676667	10037208	7f34a07.x1 cDNA, 3' end /clone=IMAGE:3296532 /clone_end=3'	-1	ACACAGATTTGAAGTCTACTGTTCTA AATGGCCTCTACTTCCTGCTGTCA

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6102	db mining	Hs.102165	BE676737	10037278	7f37g03.x1 cDNA, 3' end /clone=IMAGE:3296884 /clone_end=3'	-1	GGAACTTCTGCTTCCACTTACGATGA AGGAACTTGTACTCAATCCATCCA
6103	db mining	Hs.283276	BE676772	10037313	7f35d05.x1 cDNA, 3' end /clone=IMAGE:3296649 /clone_end=3'	-1	GAAGCCTTCCTGTGGTCATAACAAGT CTCACACACCCCAAGGACTGATCT
6104	db mining	Hs.86761	BE738569	10152561	601572850F1 cDNA, 5' end /clone=IMAGE:3839581 /clone_end=5'	-1	GAGTCCAGCCTTTGAACCTGGCGCT GAATCCTGACTTTACTGCTTATTCA
6105	Table 3A	Hs.293842	BE748663	10162655	601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5'	-1	AAACTCATACATGCAGAAAATTGTCTT TGCTCGAAATGGTAATGCCAAAA
6106	Table 3A	Hs.293842	BE748663	10162655	601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5'	-1	AAACTCATACATGCAGAAAATTGTCTT TGCTCGAAATGGTAATGCCAAAA
6107	Table 3A	Hs.270293	BE857296	10371182	7g27b01.x1 cDNA, 3' end /clone=IMAGE:3307657 /clone_end=3'	-1	ACAAAAGTCATGGCTGTGAGGCTATC ATTACCCTTTTACCAAAGTTGGAA
6108	Table 3A	Hs.155935	BE858152	10373065	complement component 3a receptor 1	-1	AGTTCTATTTCTATCCCAAACTAAGCT
8109	Table 3A	Hs.294348	BE961923	11764299	(C3AR1), mRNA /cds=(0,1448) 601655335R1 cDNA, 3' end /clone=IMAGE:3845768 /clone_end=3'	-1	ATGTGAAATAAGAGAAGCTACTTTGT ATCCCGATGGTGCCCACCGCTATTAA AGGTTCGTTTGTTCCACGATTAAA
6110	Table 3A	Hs.5181	BE962588	11765636	proliferation-associated 2G4, 38kD	-1	ATGTCTCCATACCCATTACAATCTCC
6111	Table 3A	Hs.314941	BE962883	11766238	(PA2G4), mRNA /cds=(97,1281) 602381893F1 cDNA, 5' end	-1	AGCATTCCCCCTCAAACCTAAAAA GCCCGTATTTACCCTATAGCACCCCC
9111	rabio art	110.01-10-11	DESCEDE	11100200	/clone=IMAGE:4499447 /clone_end=5'		TCTACCCCTTTAGAGCCCAAAAA
6112	Table 3A	Hs.301110	BE963194	11766612	601656811R1 cDNA, 3' end /clone=IMAGE:3865731 /clone_end=3'	-1	ACATTTTCCTCCGCATAAGCCTGCGT CAGATTAAAACACTGAACTGA
8113	Table 3A	Hs.330887	BE963374	11766792	601657137R1 cDNA, 3' end /clone=IMAGE:3866193 /clone_end=3'	-1	CCAAGCTGGTTTCAAGCCAACCCCAT GGCCTCCATGACTTTTTCCAAAAC
8114	Table 3A	Hs.334926	BE963551	11766970	Homo sapiens, clone MGC:8857 IMAGE:3866266, mRNA, complete cds /cds=(62,133)	-1	TGATCAGGTGAACCGGAAGTCTCCAA TTTCTGAATGGATTATGTTTCTAA
6115	Table 3A	Hs.316047	BE963666	11767085	601656685R1 cDNA, 3' end /clone=IMAGE:3865820 /clone_end=3'	-1	TGAGTACGTGACACTTGTTGTAGAAT AGTGGTGTTGAGCTATATTCTTGT
6118	Table 3A	Hs.294578	BE983811	11767228	601657462R1 cDNA, 3' end /clone=IMAGE:3875846 /clone_end=3'	-1	GTGACCCTTGGCACCCGCTAGAAGTT TATGGCCGAGCTTTACCAATTAAA
6117	Table 3A	Hs.302585	BE984028	11767356	601657601R1 cDNA, 3' end /clone=IMAGE:3875617 /clone_end=3'	-1	TGAACTCCAACTTTGACCAACCCATG AGACCCCTGTTATCCAAACTTTCT
8118	db mining	Hs.210828	BE964051	11767519	801472729T1 cDNA, 3' end /clone=IMAGE:3875791 /clone_end=3'	-1	CCCTCTACTATTTGGCTCCATAACTTA GGACCTGCCTTTCCCGGTTCCAG
8119	Table 3A	Hs.330588	BE984134	11767602	801151626F1 cDNA, 5' end /clone=IMAGE:3507774 /clone_end=5'	-1	CCCGTATTTACCCTATAGCACCCCCT CTACCCCCTTTAGAGCCCCAAAAA
6120	Table 3A	Hs.252259	BE984149	11767617		-1	CCAACTTTCAGAACAGAAGGGTGGG
6121	Table 3A	Hs.184052	BE964596	11768078	/cds=(22,753) PP1201 protein (PP1201), mRNA	-1	AAACCAGAACCGCCTGCCATGCCCC GCGCCAGAAATCCAATCC
6122	Table 3A	Hs.286754	BE965319	11769559	/cds=(75,1010) 601659229R1 cDNA, 3' end	-1	GGATATAGTTAGGATTAATTACTTA CTGAGATTTTGGGTTTTCCACACGGG
					/clone=IMAGE:3895783 /clone_end=3*		CCAAGATACCCGGCCTCTGCTGAG
6123	Table 3A	Hs.297190	BE965554	11770044	601659486R1 cDNA, 3' end /clone=IMAGE:3896204 /clone_end=3'	-1	ATATCATTTCCACTTAGTATTATACCC ACACCCACCCAAGAACAGGGTTTT
6124	Table 3A	Hs.108327	BF001438	10701713	damage-specific DNA binding protein 1 (127kD) (DDB1), mRNA /cds=(109,3531)	-1	ACAGCATGAGAAACTGTTAGTACGCA TACCTCAGTTCAAACCTTTAGGGA
6125	Table 3A	Hs.161075	BF001821	10702096		-1	GCTTGCCCTAGCAGAGTCATACGGAA TAATGGAAAACTCAACTTCTGTTC
6126	Table 3A	NA	BF056055	10809951	7k07h12.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3443950 3' similar to contains element L1 repetitive eleme	-1	CACAATGCTGCCTCCTCTGTGGATGA CTGATGGCAAGAGTCTGAATTGAA
6127	Table 3A	Hs.221695	BF058398	10812294	7k30d01.x1 cDNA, 3' end /clone=IMAGE:3476785 /clone_end=3'	-1	CCTCTCACTCTCAGACTCCAAGGGCC AAGAAAAACTACGGACAGGAAGCC
6128	db mining	Hs.255664	BF058429	10812325	7k30g11.x1 cDNA, 3' end /clone=IMAGE:3476949 /clone_end=3'	-1	GAGAGGAGGGTCTCAGACGTTGGG GGACACACTGCTGGGTGGGTGATTT
6129	Table 3A	Hs.43857	BF058599	10812495	mRNA for KIAA1247 protein, partial	-1	TAAGAAATCCCAATTTTCAGGAGTGG
6130	Table 3A	Hs.144583	BF059133	10813029	cds /cds=(285,2942) Homo sapiens, clone IMAGE:3462401, mRNA, partial cds /cds=(0,153)	-1	TGGTGTCAATAAACGCTCTGTGGC CGGCAGGGTGGCCTGTAACAATTTCA GTTTTCGCAGAACATTCAGGTATT

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6131	db mining	Hs.257697	BF060727	10819637	AL533532 cDNA /clone=CS0DN004YJ14-(5-prime)	-1	GGGGCTCCCTTCCCGGCTTTGTTTTC TCTGGGAGATTTTATTTT
6132	Table 3A	Hs.193237	BF062295	10821193	7k76b11.x1 cDNA, 3' end /clone=IMAGE:3481293 /clone_end=3'	-1	GAAAGTGGAGGGAGTGGACGGGGAG GAGACTAGCCAGAGAGGCTCATTAG
6133	Table 3A	Hs.174215	BF062628	10821538	7h62h05.x1 cDNA, 3' end /clone=lMAGE:3320601 /clone_end=3'	-1	CTTCTCCCCTCTTGCCCTCTGTGGTC TGATTTAAAACGAAAAGGTCGGAT
6134	db mining	Hs.159013	BF063675	10822585	hh82b10.x1 cDNA, 3' end /clone=IMAGE:2969275 /clone_end=3'	-1	GGACTTCTGAAATAGAGCTGGCTCCC TGGGGTGACAATGTATATATGCAA
6135	Table 3A	Hs.125887	BF109873	10939563	hypothetical protein FLJ14464 (FLJ14464), mRNA /cds=(69,3146)	-1	CTGGGTGTCGTGGAAGATGACGAAG ATGCTGGGCTGGCAGATGCAGTCCA
6136	Table 3A	Hs.288443	BF110312	10940002	7n36d08.x1 cDNA, 3' end /clone=IMAGE:3566654 /clone_end=3'	-1	ACCAGGGCTTAAAACCTCAATTTATG TTCATGACAGTGGGGATTTTTCTT
6137	Table 3A	Hs.250905	BF116224	10985700	hypothetical protein (LOC51234), mRNA /cds=(0,551)	-1	ATTCTCCAACCACAAACAGCACTTCT AAAACTAACTTTACTTT
6138	Table 3A	Hs.318215	BF183507	11061818	601809991R1 cDNA, 3' end /clone=IMAGE:4040470 /clone_end=3'	-1	GATATAGTCTCCATACCCCATTACCA TCTCCCAGCCATTCCCCCTCCAAC
6139	Table 3A	Hs.96566	BF194880	11081165	602137338F1 cDNA, 5' end /clone=IMAGE:4274048 /clone_end=5'	-1	TGATACTTTGGTTCTCTTTCCTGCTCA GGTCCCTTCATTTGTACTTTGGA
6140	Table 3A	Hs.232257	BF195579	11082611	RST2302 cDNA	-1	TAATACTGGAGGGGCTTGAAGAAGG CTGTCGTGTTTTGTCACCTGCTTTG
6141	Table 3A	Hs.3353	BF197153	11085769	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCTTTCCCGTCTTTCTTCCTCACCTA TGTAATTTCAGTAGTCTCTCAGC
6142	Table 3A	NA	BF197762	11087169	7p91f02.x1 NCI_CGAP_Skn1 cDNA clone IMAGE:3653139 3', mRNA sequence	-1	AGGAAGAGCCTGCACCTGTGGTGGA ACAATCAGGGAAAAGGAAGTCAAAA
	Table 3A	Hs.50785	BF221780		cerevisiae)-like 1 (SEC22L1), mRNA /cds=(119,768)	-1	TTTGGAGCTTCTATAGGAGTGGAGAG GGGCAGCTCATTGTTGAGAGTTGC
6144	Table 3A	Hs.250811	BF432643	11444806	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA /cds=(170,790)	-1	TGATCTGACTGGAAAACAATCCTGTA TCCCCTCCCAAAGAATCATGGGCT
6145	Table 3A	Hs.296358	BF433058	11445221	mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162) /cds=UNKNOWN	-1	TCATCCCTTAAACACTCTGTGATGGG ATCTTCAGGATCATCTTTTGAAGT
6146	Table 3A	Hs.76611	BF433353		601435773F1 cDNA, 5' end /clone=IMAGE:3920562 /clone_end=5'	-1	TGCGTTTGGTTTAGGAATGTGCTTTT GTACTTCCACTTGAATAAAGGTGT
6147	Table 3A	Hs.178703	BF433657	11445846	/clone=DCBBCH05 /clone_end=51	-1	TGCTCAGGGCACATGCACACAGACAT TTATCTCTGCACTCACATTTTGTG
6148	Table 3A	Hs.222833	BF435098	11447386	7p05g01.x1 cDNA, 3' end /clone=IMAGE:3845097 /clone_end=3'	-1	GGTTATTGCTGACACGCTGTCCTCTG GCGACCTGTCGCTGGAGAGGTTGG
6149	Table 3A	Hs.293476	BF435621	11447923	hypothetical protein FKSG44 (FKSG44), mRNA /cds=(126,1520)	-1	CGTTTTCTGAGCATCCGTTGTGCCTT AACATTTTCTGCTTGTCCTTTGGG
6150	db mining	Hs.257641	BF436704	11448943	7p07d12.x1 cDNA, 3' end /clone=IMAGE:3644999 /clone_end=3'	-1	CTTCTGAATGCCCGAGTCTTCTCTTT TGTGCTCACAAATGCCACCCAATC
6151	Table 3A	Hs.160980	BF437585	11449991	/clone=IMAGE:3651526 /clone_end=3*	-1	TGCTTACAAGGGTGATTGACCTTGCC TTACTCTTTATGTAAATTATGGCA
6152	db mining	Hs.258513	BF437915		AF150421 cDNA /clone=CBNBCG12	-1	CTGGCGTATTACCATTTTGATAGCCT CTCTTCAGGCTAGATAAGCTGGGG
6153	Table 3A	Hs.126594	BF445163	11510224	/clone=IMAGE:3366191 /clone_end=3*	-1	CCCTGTATTATTGAAATGTCAGCATA ATGACTGGAAGGTGAAATTGGTCC
6154	Table 3A	Hs.174104	BF445405	11510543	/clone=IMAGE:3923643 /clone_end=5*	-1	ACTGCTGTTGCATGAATAGATGATAC AAAGCAAGTGATGAGGTTGGTATG
6155	Table 3A	Hs.143389	BF446017		7p18a11.x1 cDNA, 3' end /clone=IMAGE:3646004 /clone_end=3'	-1	TGGAAGAACAAATTCAGACATCATCA GTAAGTCTTTAGGGACACAGGGAA
6156	Table 3A	Hs.295726	BF447885	11513023	alpha polypeptide, antigen CD51) (TGAV), mRNA /cds=(41.3187)	-1	AGTGAAAACTGGTACAGTGTTCTGCT TGATTTACAACATGTAACTTGTGA
6157	Table 3A	Hs.179526	BF475501	11546328	upregulated by 1,25-dihydroxyvitamin D- 3 (VDUP1), mRNA /cds=(221,1396)	-1	GCCAGAAAGTGTGGGCTGAAGATGG TTGGTTTCATGTTTTTGTATTATGT
6158	Table 3A	Hs.181311	BF478238	11549065	asparaginyl-tRNA synthetase (NARS), mRNA /cds=(73,1719)	-1	TGTCCTCTGAACCTGAGTGAAGAAAT ATACTCTGTCCTTTGTACCTGCGT
6159	Table 3A	Hs.179703	BF507849	11591147	mRNA /cds=(10,1230)	-1	CCATTTCCACTACATGCCTTTCCTAC CTTCCCTTCACAACCAATCAAGTG
6160	Table 3A	Hs.159673	BF508053	11591351	UI-H-BI4-apx-b-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3088845 /clone_end=3'	-1	ACACTTCCCTGAATGTTGAAGAAGAT ATGCTATCCATGCAATCCTTGTCG

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6161	Table 3A	Hs.158999	BF508694	11591992	UI-H-BI4-aop-f-09-0-UI.s1 cDNA, 3' end /done=IMAGE:3085601	-1	ACTTGTGTTTGAACCACTTCTGCTTC CTCTTTAACCTGAGATGCACACGT
6162	Table 3A	Hs.77542	BF508702	11592000	/clone_end=3' 602629438F1 cDNA, 5' end /clone=IMAGE:4754432 /clone_end=5'	-1	ACATTCTCTCATTTTGCTGAAGCTGAT TTGATTGGGTGTCTGTTTCTCGC
6163	Table 3A	Hs.127311	BF508731	11592029	AU185774 cDNA /done=B02302-013	-1	TGACAGAATGAACTGGAAATGAAATC
6164	Table 3A	Hs.144265	BF509758	11593056	UI-H-BI4-apg-d-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3087390 /clone_end=3'	-1	CCACAGTTATGATCGTAGTAGAGT AAGTACAGATGCCATCCCGGTGCTGT GATCTTCCAGCCATTCTCCATTTC
6165	Table 3A	Hs.256931	BF510393	11593691	zb02d05.s1 cDNA, 3' end /done=IMAGE:300873 /clone_end=3'	-1	ACTGCCAATCTGATTTAAAATTCTCCA AGCTTAATTCTGTGCAACAAACA
6166	Table 3A	Hs,276341	BF510670	11593968	UI-H-BI4-aof-b-08-0-ULs1 cDNA, 3' end /clone=IMAGE:3084615 /clone_end=3'	-1	GCCTGTTGTTCTGTTTATCGCCCTAT TTTACAAAACTGATTCTGACCTGG
8167	Table 3A	Hs.248689	BF512500	11597602	UI-H-BI3-alw-h-10-0-UI.s1 cDNA, 3' end /clone=IMAGE;3069162 /clone_end=3'	-1	AACTGGCATTGCTAAGCCCCAGAAAA ATGTATTTAGTGGAACAGATGAAA
6168	Table 3A	Hs.136375	BF513274	11598453	602544150F1 cDNA, 5' end /clone=IMAGE:4666332 /clone_end=5'	-1	ACACTAGGTCCTTTTATACCTGTGCC TTTACGTTCGTTTTCCTGATTGCA
6169	Table 3A	Hs.300870	BF513602	11598781	mRNA; cDNA DKFZp547M072 (from clone DKFZp547M072) /cds=UNKNOWN	-1	AATACAGATTCATTTTATTTAAGCGTC CGTGGCACCGACAGGGACCCCAG
6170	Table 3A	Hs.255340	BF514247	11599426	UI-H-BW1-ani-h-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082601 /clone_end=3'	-1	AGTTCATCCCCTTTCAGAAGCTGTTT GCTCTTGGCTCATTAAACCTGTGA
8171	Table 3A	Hs.283022	BF514341	11599520	triggering receptor expressed on myeloid cells 1 (TREM1), mRNA /cds=(47,751)	-1	GCCTCTTTTCCTGTATCACACAAGGG TCAGGGATGGTGGAGTAAAAGCTC
6172	Table 3A	Hs.83734	BF515538	11600717	syntaxin 4A (placental) (STX4A), mRNA /cds=(66,959)	-1	TGTTAGGTGGCCTCTGCATACCTATG GGAACTCAGTGATGTAATGCAAAG
8173	Table 3A	Hs.146065	BF591040	11683364	AL580165 cDNA	-1	CTGGGGCCGTAGCAAAAATCATGAAA
8174	Table 3A	Hs.30941	BF592138	11684462	/cione=CS0DJ005YB18-(3-prime) calcium channel, voltage-dependent, beta 2 subunit (CACNB2), mRNA /cds=(501,2318)	-1	AACACTTCAACGTGTCCTTTCAAT TGCCAAGTCAGCAGATTTGCTTTATG AATTACAGGGACTAGAAATGCCCA
8175	Table 3A	Hs.695	BF690338	11975746	cystatin B (stefin B) (CSTB), mRNA /cds=(96,392)	-1	TTGCATGTCTCTTCCTAAATTTCATTG TGTTGATTTCTAATCCTTCCCGT
6176	Table 3A	Hs.142838	BF732404	12057407	nucleolar protein interacting with the FHA domain of pKi-67 (NIFK), mRNA /cds=(54,935)	-1	AGAGTGAGAAGGCAGTTCCAGTTTTA GCACAGATTTGTTTATGTGTTCAG
6177	Table 3A	Hs.296317	BF938959	12356279	mRNA for KIAA1789 protein, partial cds /cds=(3466,4899)	-1	GAAGTGACACTGACTGTATCTACCTC TCCTTTTCTTCATCAGGTGTTCCT
6178	Table 3A	Hs.182937	BF939014	12356334	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(44,541)	-1	TCCCTGGGTGATACCATTCAATGTCT TAATGTACTTGTGGCTCAGACCTG
8179	Table 3A	Hs.26136	BF940103	12357423	hypothetical protein MGC14156 (MGC14156), mRNA /cds=(82,426)	-1	AATTCCAAAGGAGTGATGTTGGAATA GTCCCTCTAAGGGAGAGAAATGCA
8180	Table 3A	Hs.133372	BF940291	12357811		-1	AGCCCTCCACCCCACCCAGTACTTT TACAATGTGTTATTAAAGACCCCT
6181	Table 3A	Hs.304900	BF980139	12347354	602288147F1 cDNA, 5' end /done=IMAGE:4373963 /clone_end=5'	-1	CCATCCTTGAGAAATGTGGGCACCAA GTCCATAAATCTCCATAAATCCAAT
6182	Table 3A	Hs.303214	BG054649	12511438	7o45b01.x1 cDNA, 3' end /clone=IMAGE:3576912 /clone_end=3'	-1	CGTTGCATTTTCACATTTGTGGCA GGACAAGCATGGGGCAAGAGGGAC
6183	Table 3A	Hs.8258	BG054966	12512220	cDNA FLJ14737 fis, clone NT2RP3002273, weakly similar to SCD6 PROTEIN /cds=(77,1468)	-1	TATGAGTTTATGCGTTTTCCCAGCCC TCCGAATCACTGACTGGGGCGTTT
6184	Table 3A	Hs.179661	BG056668	12521375	Homo sapiens, tubulin, beta 5, clone MGC:4029 IMAGE:3617988, mRNA, complete cds /cds=(1705,3039)	-1	TTGAAAAGATGACATCGCCCCAAGAG CCAAAAATAAATGGGAATTGAAAA
6185	Table 3A	Hs.56205	BG057282	12522612	insulin induced gene 1 (INSIG1), mRNA /cds=(414,1247)	-1	TGCACTCTACCAGATTTGAACATCTA GTGAGGTTCACATTCATACTAAGT
6186	Table 3A	Hs.3709	BG057892	12523835	low molecular mass ubiquinone-binding protein (9.5kD) (QP-C), mRNA /cds=(77,358)	-1	TGGTGATATCTGCTTAGATTTCCCTG TATCTTTGCTGCCCTCCTTCAAGT
6187	Table 3A	Hs.5122	BG058599	12525258	602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5'	-1	AGTTGGAGCTATCTGTGCAGCAGTTT CTCTACAGTTGTGCATAAATGTTT
6188	Table 3A	Hs.89104	BG058739	12525527	602590917F1 dDNA, 5' end /done=IMAGE:4717348 /clone_end=5'	-1	CGTGGGAGGATGACAAAGAAGCATG AGTCACCCTGCTGGATAAACTTAGA
6189	Table 3A	Hs.166982	BG149747	12661777	phosphatidylinositol glycan, class F (PIGF), mRNA /cds=(67,726)	-1	GTGGTTTGGTCAGCATACACACTTCT CATTTCATTTGATGTACACAGCCA
6190	Table 3A	Hs.100293	BG149986	12662016	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N- acetylglucosamine:polypeptide-N- acetylglucosamimy transferase) (OGT).	-1	ACCTGGGATTTCATTTCTGCTGAAAG AAATAGGAAGAACAGGACTCACTT
					mRNA /cds=(2039,4801) 529		

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6191	Table 3A	Hs.198427	BG150273	12662303	hexokinase 2 (HK2), mRNA /cds=(1490,4243)	-1	GGGTGTGATGAATAGCGAATCATCTC AAATCCTTGAGCACTCAGTCTAGT
6192	Table 3A	Hs.313610	BG150461	12662491	7k01d08.x1 cDNA, 3' end /clone=IMAGE:3443006 /clone_end=3'	-1	AGCTTTCACCACCTCGCAGTTGTAGA GATAGTCCCCGAAATATTATTCCA
6193	Table 3A	Hs.184456	BG230563	12725596	hypothetical protein (LOC51249), mRNA /cds=(0,611)	-1	GTGTGAAGTGACAGCCTTGTGTGTGA TGTTTTCTGCCTTCCCCAAGTTTG
6194	Table 3A	Hs.89104	BG231557	12726664	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TTGTTTTAACAACTCTTCTCAACATTT TGTCCAGGTTATTCACTGTAACCA
6196	Table 3A	Hs.152925	BG231805	12726934	mRNA for KIAA1268 protein, partial cds /cds=(0,3071)	-1	TAAGTGGATTGGCAGACTCCTTGTTG CTTAAGAGTGGCTTTCTAGGCAGG
6196	Table 3A	Hs.89104	BG231961	12727100	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TTGTTTTAACAACTCTTCTCAACATTT TGTCCAGGTTATTCACTGTAACCA
6197	Table 3A	Hs,337986	BG235942	12749789	Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336.1494)	-1	GCCAGTCTCTATGTGTCTTAATCCCT TGTCCTTCATTAAAAGCAAAACTA
6198	Table 3A	Hs.3353	BG236015	12749862	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCTTTCCCGTCTTTCTTCCTCACCTA TGTAATTTCAGTAGTCTCTCAGC
6199	Table 3A	Hs.75703	BG236084	12749931	small Inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	-1	GGTCCACTCTCACTCTTTCTCTGCTG TTGCAAATACATGGATAACACCGT
6200	db mining	Hs.5146	D19756	500072	HUMGS00712 cDNA, 3' end /clone=mm0970 /clone_end=3'	-1	CATTCAGTATTTATTGGGAAGACTTG TCAAGCACCATGATAAGTGGTGGA
6201	db mining	Hs.237971	D19770	500086	hypothetical protein MGC5627 (MGC5627), mRNA /cds=(72,584)	-1	AGAGGGGAAGGACTTACATGACAT CCTACTGGGAATTTGCTAGAAACCA
6202	db mining	Hs.30709	D20225	501322	HUMGS01199 cDNA, 3' end /clone=pm0880 /clone_end=3'	-1	CTGGTGAAGCTGACTCCCCAGGTAAA GAGATATCAGCTCTGCTTCAGACT
6203	db mining	Hs.30731	D20378	501474	HUMGS01352 cDNA, 3' end /clone=pm2943 /clone_end=3'	-1	TTGCTTCTTCCTGCTTTATAGAGTTCC CGTAAAATACCCTTCACCCTGGC
8204	db mining	NA	D20425	501521	HUMGS01399 Human promyelocyte cDNA clone pm1281 3', mRNA sequence	-1	TCTGACCTCCGTGACGTTTATTACCA GCTGATGTCCCGTACACTGATTTCA
	db mining	Hs.229071	D20458	501554	HUMGS01432 cDNA, 3' end /clone=pm1542 /clone_end=3'	-1	GGGAAGGGTCAGCAACGATTTCTCA CCAAATCACTACACAGACACAAAGG
6206	db mining	Hs.330221	D20485	501561	HUMGS01439 cDNA, 3' end /clone=pm2194 /clone_end=3'	-1	ACCACTAAATGGTTACACTACACCAA GACACTAAAATGGCAGGGAGCCCT
6207	db mining	Hs.92440	D20522	501618	HUMGS01497 cDNA, 3' end /clone=pm1507 /clone_end=3'	-1	AAATTCAAATCACCCTTGATACCCAC TTCTTTCTCCCACCCAAATCTGAT
8208	db mining	Hs.90165	D20538	501634	HUMGS01513 cDNA, 3' end /clone=pm1504 /clone_end=3'	-1	ACCATATCGTGCAAAATGTAATATGG AATTTCCAAACATCAATGAAGGGAT
6209	db mining	Hs.90171	D20572	501668	HUMGS01547 cDNA, 3' end /clone=pm1503 /clone_end=3'	-1	AATAAGTACCGTATATAAACACTTCTC TTTCTCTCCTCCACAATGGCACG
6210	db mining	Hs.30766	D20726	504546	HUMGS01703 cDNA, 3' end /clone=mp0664 /clone_end=3'	-1	AGCATCACTCTTAGAAGAAGCAACTC CTTCCCTTGATTCTGTGTATTTGG
6211	db mining	Hs.5816	D20040	504666	HUMGS01827 cDNA, 3' end /ctone=mp0825 /ctone_end=3'	-1	TCAACCCAGAATCTATAATGTATGAA ATAAATTAATAGAGAACCCAACAGAT C
6212	db mining	Hs.30793	D20888		HUMGS01869 cDNA, 3' end /clone=mp0836 /clone_end=3'	-1	AAGGTCTCCATCTAACAGGTAGAGCA GTTGGTGCAGATGAGATG
6213	Table 3A	Hs.292590	D59502	960608	602626586F1 cDNA, 5' end /clone=IMAGE:4751396 /clone_end=5'	-1	GGTGATGATACCACCTCCAATGAACA GGGAAGCAAGTTCATCAGTCAACA
8214	Table 3A	Hs.119274			RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4- binding protein) (GAP1IP4BP), mRNA /cds=(46,2550)	-1	AGCTGTTGGGGCTGCACTGAGCTGC AATTTTTAACATGGATTTATAACTT
6215	db mining	Hs.238797		872737 ⁻	602081661F1 cDNA, 5' end /clone=IMAGE:4245999 /clone_end=5'	-1	AAGGAATTTGTTTTCCCTATCCTAACT CAGTAACAGAGGGTTTACTCCGA
6216	db mining	Hs.11307	H09541	874363	RST29274 cDNA	-1	CGCACACATTTTCTGTATGGACAAAT CCTGGATTGGCTTCGTTATTTGGT
6217	Table 3A		H69141	1030426	EST375312 cDNA	-1	GGTAATGAAACAATCATCCAGTTAAC AATCAGCAAGGTTCTTCAGAGCCT
	Table 3A		H71236	1043052	sialic acid binding tg-like tectin 5 (SIGLEC5), mRNA /cds=(142,1797)	-1	TGGAAGAGTGGACTGAAGAAGAACT TATACTCTCCCTCCTCTAAAATTGA
	Table 3A	NA	H78395	1056484	yu12f03.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:233597 3' similar to contains Alu repet	-1	TCCTGGGCTATTGGCTTTATGATATC TTTTGAGAAACAGGATTTTCACTT
	Table 3A	Hs.38664	H80108	1058197	IL0-MT0152-061100-501-e04 cDNA	-1	ACCTTTTAAGGATGTCTTATTTCCACC CCAACTCTCCACTCCA
6221	Table 3A	NA	H92914	1099242	yt94g03.s1 Scares_pineal_gland_N3HPG cDNA clone IMAGE:231988 3', mRNA sequence	-1	GAACCTTCAAAACTGTCACTTTGAGT TCCAGAAGAGTCCTTCAGCATCTT
6222	Table 3A	Hs.2210	L40410	703109	thyroid receptor interactor (TRIP3) mRNA, 3' end of cds /cds=(0,458)	-1	GTATTTGGGCTTCTCCAAGCAGATCA CGCAGACGACGGTGCTACATTTGA
6223	Table 3A	Hs.2200	L40557	705359	perforin 1 (preforming protein) (PRF1), mRNA /cds=(0,1667)	-1	CAAGCATACTGGTTCTTTCCAAGCTC ACTGTTCTCACCACACGGCCCCAC

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6224	Table 3A	Hs.198726	M24069	181483	vasoactive intestinal peptide receptor 1	-1	TCCATATCCATTTCTGACGTTGAACC
6225	Table 3A	Hs.132911	N20190	1125145	(VIPR1), mRNA /cds=(56,1543) MR2-OT0079-290500-007-b03 cDNA	-1	ATTTGACAGTGCCAAGGACTTTGG AAGCCTGTTTTTCACTCTAAAAATTCA
6226	Table 3A	Hs.323950	N23307	1137457	zinc finger protein 6 (CMPX1) (ZNF6),	-1	AGAGGACACGCTAAGAACGATCA CCTCAGCTTCCAACTCTGATTCCAGG
6227	Table 3A	Hs.32250	N30152	1148672		-1	ACAGGATGGAAAACCTTTGGACAG GCGCACATGGCTATTTTGATACACAA
6228	db mining	Hs.44512	N33584	1153983	/clone=IMAGE:268157 /clone_end=3' yv21f11.s1 cDNA, 3' end	-1	AGTTGTGTTTGCTACTTTAGAAGC AACTCACGACAATTGCTACAAAACAC
6229	Table 3A	Hs.3353	N36787	1157929	/clone=IMAGE:243405 /clone_end=3' beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1),	-1	CAGGGAGGGCTTTTTGTGTTTTT GTCTTTCCCGTCTTTCTTCCTCACCTA TGTAATTTCAGTAGTCTCTCAGC
6230	Table 3A	Hs.38218	N39230	1162437	mRNA /cds=(175,1179)	-1	GCCCTGGTATGTATGCCTTTCTCCC TACTGTCTAATAGCACCTCGTAAA
6231	Table 3A	Hs.236456	N49836	1191002	602287746T1 cDNA, 3' end /clone=IMAGE:4375067 /clone_end=3'	-1	AAGAAACCGTGGAAGATACTGGTTTA TTTCAAATGAGCAGAGTATGTTGT
6232	Table 3A	Hs.114453	N58052	1201942	601880526F1 cDNA, 5' end /clone=IMAGE:4109119 /clone_end=5'	-1	CCACCTCTTCTGACATGAATGTAGCA TAAGTTAGCAATCGGTTCTTCCAA
6233	Table 3A	Hs.334731	N58136	1202026	Homo sapiens, clone IMAGE:3448306, mRNA, partial cds /cds=(0,2353)	-1	AGGTTCCCTTTCAAATAAAGATAAAG AATTTGACTTGGGACACTGCCAGA
6234	Table 3A	Hs.205555	N72600	1229704	za46f08.r1 cDNA, 5' end /clone=IMAGE:295623 /clone_end=5'	-1	GGCTGGCCTCATTTTGAAAAGTTAGT ACAATTTTCTTCAGTGCTAACTTG
8235	Table 3A	Hs.256931	N80578	1243279	zb02d05.s1 cDNA, 3' end /clone=IMAGE:300873 /clone_end=3'	-1	ACTCCAGAACGTCAGAAATGGTGTAG CAGAATGAATTCTGTTATAAGGAA
6236	Table 3A	Hs.303018	N94511	1266820	zb80g04.s1 cDNA, 3' end /clone=IMAGE:309942 /clone_end=3'	-1	CTGTTCGAAAGTTGGAGACTGCCTGT ACCCAGGTTGATAGTCAATTGTTT
6237	db mining	Hs.118984	NM_017660	8923093	hypothetical protein FLJ20085 (FLJ20085), mRNA /cds=(62,655)	-1	CCACCTTGAGCGCCTTCTTCTGGTTG GTTGTCATGCAGTTCTCACACATG
6238	Table 3A	Hs.11594	R12665	765741	yf40a04.s1 cDNA, 3' end /clone=IMAGE:129294 /clone_end=3'	-1	ACCCTTCCCCTTTTTCATATCCTTTCT TCAAAAATCTAAATGATGTGCCT
8239	db mining	Hs.108082	R40823	821181	602068988F1 cDNA, 5' end /clone=IMAGE:4067972 /clone_end=5'	-1	AGTTCCAGGAGGTGGTTTTAAATATT GGATGAAAACTTACAGGCTGTTTT
6240	db mining	Hs.94881	R50838	812740	602387586F1 cDNA, 5' end /clone=IMAGE:4516388 /clone_end=5'	-1	ACAATACATTTACAAAGCCATCTTTAC ATGCATTAAACGAGGGCTACAAC
8241	Table 3A	Hs.94881	R50838	812740	602387586F1 cDNA, 5' end /clone=IMAGE:4516388 /clone_end=5'	-1	ACAATACATTTACAAAGCCATCTTTAC ATGCATTAAACGAGGGCTACAAC
8242	RG housekeeping genes	Hs.92004	R52541	814443	HSU55967 cDNA /clone=39883	-1	GGCCTGAAGAAGGAGATAAGTGTTC CATTCGGCAACATAAGAGAAGTTAA
8243	RG housekeeping genes	Hs.28768	R60313	831008	602270716F1 cDNA, 5' end /clone=IMAGE:4359027 /clone_end=5'	-1	TCCATCCCAAAGGAGAGCTACTGTAC TGACTGTACTTGTGGAATGCAGCG
8244	db mining	Hs.330530	T25714	563034	ESTDIR309 cDNA, 3' end /clone=CDDIRX9 /clone_end=3'	-1	ACCCACCACTCTCAGGACCACCTGAA GGCAGAATAAACCGGATCCTGTTG
6245	db mining	NA _	T25727	583047	ESTDIRX51 CD34+DIRECTIONAL cDNA clone CDDIRX51 3', mRNA sequence	-1	AAATTGTGTGAGAAGGCTGATAAACG TCTGTGGTTTCTCCCTGTGCTATT
8246	db mining	Hs.7569	T26893	567784	ESTDIR465 cDNA, 3' end /clone=CDDIR465 /clone_end=3'	-1	GCTGGGCTTCTGCAAAATTATAAAGT TGCTTTATTAAATTCATACATGCGG
6247	db mining	Hs.172822	T26903	567794	ESTDIR551 cDNA, 3' end /clone=CDDIR551 /clone_end=3'	-1	AGCTGATTCATTCATTCTATGTGTGC CACTAAATAAAGAGATTGAGCAAGT
6248	Table 3A	Hs.185675	T98171	747516	QV2-EN0098-010201-603-a05 cDNA	-1	CTTGAAGCTGTGTTGGTGGCCTGTGA CCTTCCAATGCAATCTAGACTGTG
6249	Table 3A	Hs.58066	W72392	1382348	602389077F1 cDNA, 5' end /clone=IMAGE:4517875 /clone_end=5'	-1	CTCATACACTTCTCAGCCTCAGCACC TAACCCTCACACACACACTCCAGTA
6250	Table 3A	NA	W86427	1400194	zh61c11.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA done IMAGE:416564 3', mRNA sequence	-1	TGAGTATTGTTGTGGGGCCGGGTAT GTCTGTATATAAATCTGTGCAGCCA
6251	Table 1	NA	AA136584	1697794	zn95b02.s1 Stratagene fetal retina 937202 cDNA clone IMAGE:565899 3', mRNA sequence	-1	AACATATCCAGGGAGGACAAACTCTG GGCTGGACAATGTATCCACAAGGG
6252	Table 1	NA	AA431959	2115667	zw77a03.s1 Soares_testis_NHT cDNA clone IMAGE:782188 3', mRNA sequence	-1	AGAGCAAGTCTCAGAAATAATGCTGT ATCTACACTGTCATGTATTTGCCA
6253	Table 1	NA	AA482019	2209697	zu98e04.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:746046 3', mRNA sequence	-1	ACCACCAGCTATTTGTAATTCCTTCTT CTAAGGCATAGTGAAAACTTGCT
6254	Table 1	NA	AA524720	2265648	ng42e03.s1 NCI_CGAP_Co3 cDNA clone IMAGE:937468 3', mRNA sequence	-1	GGACGGTTGGCTGAATGGCAACAGT GATGGAATATTTATATTTAGCCACA

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6255	Table 1	Hs.57787	AA588755	2402486	602381381F1 cDNA, 5' end /clone=IMAGE:4498845 /clone_end=5'	-1	AGGTTGTTATCAGGTGGCACAAATTA AATCCATCTTGAAGACTTCACACA
6256	Table 1	NA	AA628833	2541220	af37g04.s1 Soares_total_fetus_Nb2HF8_9w cDNA clone IMAGE:1033878 3', mRNA sequence	-1	GACTCGTTACGCCGTAGTTTGTCCTA TCTTGTTTATCAAATGAATTTCGT
6257	Table 2	Hs.180669	AA633203	2556617	OS-4 protein (OS-4) mRNA, complete cds /cds=(305,1156)	-1	AGAGCTATGGGTGCTACAGGCTTGTC TTTCTAAGTGACATATTCTTATCT
6258	Table 1	Hs.239489	AA639796	2563575	TIA1 cytotoxic granule-associated RNA- binding protein (TIA1), transcript variant 2, mRNA /cds=(185,1345)	-1	ACCCTTATAAACCAGAGCCCAGGAAA GACAGCTCGAGTGTATAATTCTCT
6259	Table 1	Hs.29282	AA748714	2788672	mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA /cds=(83,1963)	-1	AGCTCCTCCCTCTCAACACCCAGTTT CCTTGGGAGTTGTCATTAAAGGAA
6260	Table 1	Hs.111554	AA806222	2874972	ADP-ribosylation factor-like 7 (ARL7), mRNA /cds=(14,592)	-1	GCTGTAATTCTCTGTCTCATCATCCTT
6261	Table 1	NA	AA806766	2875516	ob91d04.s1 NCL_CGAP_GCB1 cDNA clone IMAGE:1338727 3', mRNA sequence	-1	TCGCTTTCTAACTGATTCCATTCCAC CATGTCAGATACTCCTGGGCTGCT
6262	Table 1	Hs.226755	AA909983	3049273	RC1-UT0033-250800-022-h02 cDNA	-1	ATCCAAGCTTTAATTCTGCCATCTCA GAATGGTGATAAACCATTTCTCCC
6263	Table 1	Hs.50252	AA984245	3162770	mitochondrial ribosomal protein L32 (MRPL32), mRNA /cds=(46,612)	-1	TCAGCCAACCTGAATCTGGTATCTTT ACTTAAACACAGCAGCTTGTAGTTA
6264	Table 1	Hs.53542	AI084224	3422647	chorea-acanthocytosis (CHAC) mRNA, complete cds /cds=(260,9784)	-1	TCAATAGTTGTGAAATTCTTCTCAGG CTCCTTAAACCCTCGCTTTGTTGT
6265	Table 1	Hs.135167	Al091533	3430592	AV712376 cDNA, 5' end /clone=DCAAND12 /clone_end=5'	-1	AGAGGCAACACTTAAACACTAGGGCT ACTGTGGCATCTATGTAGACAGGA
6266	Table 1	Hs.11637	Al275205	3897479	602388093F1 cDNA, 5' end /clone=IMAGE:4517086 /clone_end=5'	-1	TGACTTTCAGGAATGTCAGCATTGAC CTCTCCTTGCCACTGTTACTCAGC
6287	Table 1	Hs.8724	Al298509	3958245	serine threonine protein kinase (NDR), mRNA /cds=(595,1992)	-1	TCTCAAGAGAGAACGCCACAGCAGA GAGACCCAATCCGCCTAAGTTGCAG
6288	Table 1	Hs.142838	Al299573	3959158	nucleolar protein interacting with the FHA domain of pKi-67 (NIFK), mRNA (cds=/54.935)	-1	AGAGTGAGAAGGCAGTTCCAGTTTTA GCACAGATTTGTTTATGTGTTCAG
6289	Table 1	Hs.100555	Al352690	4089896	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated) (DDX18), mRNA /cds=(71,2083)	-1	GGGGTAGGAAGAGGATTGAG ATGTTTGAGCCTCATTTACATCAAT
6270	Table 1	Hs.108124	Al362793	4114414	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	-1	GCTCGCTACCAGAAATCCTACCGATA AGCCCATCGTGACTCAAAACTCAC
6271	Table 1	Hs.134342	Al363001	4114622	mRNA for LanC-like protein 2 (lancl2 gene) /cds=(186,1538)	-1	GACGCGCACACACCTTGAGTGACAG CGACCTCTTCTCTACAGGTTTTCCC
6272	Table 1	Hs.192427	Al380016	4189869	602296277F1 cDNA, 5' end /clone=IMAGE:4390770 /clone_end=5'	-1	ACTTCCCCTTTAGGTATCCCTGGAGT AATAATGACAACAAAATTCACTGC
6273	Table 2	Hs.158976			UI-H-Bl2-ahi-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2726692 /clone_end=3'	-1	GTCCTTTGATAGCAGAACAAGAGGCT CTGTGATCCTCTGGACCTCAGATT
	Table 1	NA	Al392705		tg23b03.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2109581 3*, mRNA sequence	-1	TGCAGGCTCATTGTGCTCCTTCTTCT GGGTTTCAATTGGATTTCAGTCCT
	Table 1	Hs.76239	Al393970	4223517	(FLJ20608), mRNA /cds=(81,680)	-1	GAGGACTGGGACCGTGATTCCACTA ACCGGAAACCGTCGCCTTTCGGGCC
6276	Table 1	Hs.79968	Al419082	4265013	splicing factor 30, survival of motor neuron-related (SPF30), mRNA /cds=(0,716)	-1	GGATGTGTGATGTTTATATGGGAGAA CAAAAAGCTGATGTATAGCCCTGT
	Table 1	Hs.121973		4311318	/clone=IMAGE:4547239 /clone_end=5*	-1	CCTGCAACAGCTAAGGCCAAGCCAA ACTTACCGTGGACTCAAACACTTTG
	Table 1	Hs.342008	Al498316	4390298	UI-H-Bl1-aeq-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2720186 /clone_end=3'	-1	GCCAGAATGGTACAGAGTGGAGGGT GTTCTGCTAATGACTTCAGAGAAGT
	Table 1	Hs.194054	Al523854	4437989	HA0669 cDNA	-1	GACAAAATAGTTACCTATGCTTTCCTT CTGGCACCCCGAATGTACGCAGG
6280	Table 1	Hs.14623	Al571519	4534893	interferon, gamma-inducible protein 30 (IFI30), mRNA /cds=(40,951)	-1	AAGCCCAGATACACAAAATTCCACCC CATGATCAAGAATCCTGCTCCACT
6281	Table 1	Hs.278554	Al627495	4664295	chromobox homolog 3 (Drosophila HP1 gamma) (CBX3), mRNA /cds=(111,662)	-1	TGCTGAAAGTGGTCCCAAAGGGGTA CTAGFTTTTAAGCTCCCAACTCCCC
	Table 1	Hs.17132	Al633798	4685128	602326676F1 cDNA, 5' end /clone=IMAGE:4427970 /clone_end=5'	-1	GCAACTGTTTTCTAGGACATGTTTAC TAGAACTACTTTAAGTATGCTGTGC
	Table 1	Hs.4283	Al651212		602621616F1 cDNA, 5' end /clone=IMAGE:4755315 /clone_end=5'	-1	ACAGTTACTTTGGAGCTGCTAGACTG GTTTTCTGTGTTGGTAAATTGCCT
	Table 1	Hs.324507		4888281	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(182,2056)	-1	CGCCAGAGGTCAGAACATGTCTATTT TGAATTGGATCGTTACAAATGAGC
6285	Table 1	Hs.90744	Al684022	4895316	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA /cds=(0,1268)	-1	TTCTGACACGATTACACAACGAGGCT TTAATGCCATTTGGGTAGGTGAGC
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6286	Table 1	NA	Al688560	4899854	wd39f08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2330535 3', mRNA	-1	ACTGAAAAGTTGAAAGACTTTTGCAG TGAACATTTATATAACTCCCCGCT
6287	Table 1	Hs.177708	A1697756	4985656	sequence 602369210F1 cDNA, 5' end /clone=IMAGE:4477370 /clone_end=5'	-1	TGGTTCCTGTGCTCACCATAGGGCTG GTGTACATTGGGCCATTAATAAAC
6288	Table 1	Hs.80887	AI701165	4989065	v-yes-1 Yamaguchì sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297,1835)	-1	TCTGGGAAAGACATTTTTAAGCTGCT GACTTCACCTGCAAAATCTAACAG
6289	Table 1	Hs,299883	Al742850	5111138	hypothetical protein FLJ23399 (FLJ23399), mRNA /cds=(282,1769)	-1	TGTTTTACCTCACTGTTGGACATACAT TCCAAGCTTTTCAACTCTAGGAG
6290	Table 1	Hs.14373	AI760353	5176020	yx26h11.r1 cDNA, 5' end /clone=IMAGE:262917 /clone_end=5'	-1	TITATCTCAGAATCTTGATGAACTCTG AAATGACCCCTGATGGGGGCATG
6291	Table 1	Hs.36137	Al765153	5231662	hepatocyte nuclear factor 3, gamma (HNF3G), mRNA /cds=(0,1043)	-1	CCGGGAAGCGGGGTACTGGCTGTGT
6292	Table 1	Hs.195175	Al802547	5368019	mRNA for CASH alpha protein /cds=(481,1923)	-1	AGCCCTTTCTTGTTGCTGTATGTTTA GATGCTTTCCAATCTTTTGTTACT
6293	Table 1	Hs.25648	Al803065	5368537	tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), mRNA /cds=(47,880)	-1	GGGGTATGGTTTAGTAATATCCACCA GACCTTCCGATCCAGCAGTTTGGT
6294	Table 1	NA	Al807278	5393844	wf38h03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2357909 3', mRNA sequence	-1	CTCTACCATAAGGCACTATCAGAGAC TGCTACTGGAGTGTATATTTGGTT
6295	Table 1	Hs.220850	Al880607	5554656	ym91d11.rl cDNA, 5' end /clone=IMAGE:166293 /clone_end=5'	-1	TGGGGCACTTTGAAAACTTCACAGGC CCACTGCTGCTTGCTGAAATAAAA
6296	Table 1	Hs.23096	Al884671	5589835	602254146F1 cDNA, 5' end /clone=IMAGE:4346626 /clone_end=5'	-1	TGGCGAGGATAAATAGAGGCATTGTT TTTGCTACTTTGCATATCATTGGC
6297	Table 1	Hs.179391	Al917642	5637497	wi52d11.x1 cDNA, 3' end /clone=IMAGE:2393877 /clone_end=3'	-1	GCAGGAAAGATGGGGTGGTGGACTG TTTTTGCCTACTTTTTGTTTTTGAA
8298	Table 1	Hs.180446	Al948513	5740823	importin beta subunit mRNA, complete cds /cds=(337,2967)	-1	CAGGGTATCAGATATTGTGCCTTTTG GTGCCAGGTTCAAAGTCAAGTGCC
8299	Table 1	Hs.7557	AL042081		FK506-binding protein 5 (FKBP5), mRNA /cds=(153,1526)	-1	AGGCTGCATATGGATTGCCAAGTCAG CATATGAGGAATTAAAGACATTGT
8300	Table 1	Hs.39911	AL138429		mRNA for FLJ00089 protein, partial cds /cds=(62,1111)	-1	TTAAGAACCCCAAAGATTAAAGGAAA CAATGTTAAGGGCTTTTGTGAGGA
6301	Table 1	Hs.13144			HSPC160 protein (HSPC160), mRNA /cds=(53,514)	-1	GATACACTGTCCAGCCCAGGTCCAG GCCCTAGGTTCTTTACTCTAGCTAC
8302	Table 1	Hs.28670			AL540260 cDNA /clone=CS0DF032YF03-(3-prime)	-1	ACTCAGGTGGTGCTGGTGTTAGTGAT GCTGGAGAAGAGAA
8303	Table 1	Hs.183232			hypothetical protein FLJ22638 (FLJ22638), mRNA /cds=(12,476)	-1	AAACACAGCCCACCCCATTTCAGACC GCCTTCCTGAGGAGAAAATGACAG
6304	Table 1	Hs.5057			AL578975 cDNA /clone=CS0DK012YN01-(3-prime)	-1	TTGGCCCAGTGTGATTGATTGCTTTA TCTTTGGTACTTTTACTTGAATGG
6305	Table 1	Hs.198298	AL582354	12950255	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), mRNA /cds=(297,5015)	-1	AGCCTGAGGCAAATAAAATTCCAGTA ATTTCGAAGAATGGGTGTTGGCAA
6306	Table 1	Hs.101370	AL583391	12952309	AL583391 cDNA /clone=CS0DL012YA12-(3-prime)	-1	AGGACCTTGACAAGCCGTTTGAGATG- GAATGTAGGCCCTGATGTTATGCT
6307	Table 1	Hs.38218	AV659358	9880372	602569369F1 cDNA, 5' end /clone=IMAGE:4693744 /clone_end=5'	-1	TGTAAGTTGACTTTCAAAAGTCTCTG GAAACACTGGACTTTAGCTGGTCC
6308	Table 1	Hs.301704	AW002985	5849991	eomesodermin (Xenopus laevis) homolog (EOMES), mRNA /cds=(0,2060)	-1	AACAAGCCATGTTTGCCCTAGTCCAG GATTGCCTCACTTGAGACTTGCTA
6309	Table 1	NA	AW027160	5885916	wt72b08.x1 Soares_thymus_NHFTh cDNA clone IMAGE:2512983 3' similar to contains Alu repetitive eleme	-1	ACCGCCAAAGCCAATCATCCACTTTC AGTACTTACCTAACCAATCTCCCA
6310	Table 1	Hs.89433	AW071894	6026892	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 1, mRNA /cds=(196,4791)	-1	TTTGGGGGATCCTTTTGTAATGACTT ACACTGGAAATGCGAACATTTGCA
6311	Table 1	Hs.335449	AW136717	6140850	UI-H-Bi1-adm-a-03-0-UI.s1 cDNA, 3' end /clone=iMAGE:2717092 /clone_end=3'	-1	TTCTGGCCTTGTTCACCTAGAAACGC TATTTCCTGTGTTATGGTTCTGGC
6312	Table 1	Hs.12035	AW137149	6141282	602122419F1 cDNA, 5' end /clone=IMAGE:4279300 /clone_end=5'	-1	GGGTTACATITGAGTCTCTGTACCTG CTTGGAAGAAATAAAAATACGTGT
6313	Table 1	Hs.337727	AW161820	6300853	au70h03.x1 cDNA, 3' end /clone=IMAGE:2781653 /clone_end=3'	-1	TGTGGGCTTGGTATAAACCCTACTTT GTGATTTGCTAAAGCACAGGATGT
6314	Table 1 ·	Hs.81248	AW166442	6397967	CUG triplet repeat, RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585)	-1	ACTGGCAAATGAAGCATACTGGCTTG CAGGGACCTTCTGATTCAAGTACA
	Table 1		AW293159	6699795	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(218,541)	-1	CTCCCATCATTCCCTCCCGAAAGCCA TTTTGTTCAGTTGCTCATCCACGC
6316	Table 1	Hs.328348	AW338115	6834741	tp39g05.x1 cDNA, 3' end /clone=IMAGE:2190200 /clone_end=3'	-1	GGCGTTTCCCATTGACCAGTTTGACC CTGGTTTGAATAAAGAGAAGTGCG

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6317	Table 1	Hs.337986	AW440517	6975823	Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds	-1	GCCAGTCTCTATGTGTCTTAATCCCT TGTCCTTCATTAAAAGCAAAACTA
6318	Table 1	Hs.250	AW444632	6986394	/cds=(1336,1494) xanthene dehydrogenase (XDH), mRNA /cds=(81,4082)	-1	TGCAATGAGGCAGTGGGGTAAGGTT AAATCCTCTAACCGTCTTTGAATCA
6319	Table 2	Hs.335815	AW444812	6986574	UI-H-Bi3-ajy-d-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733380 /clone_end=3'	-1	TGGCAACTTCAACTCCTTGATGGCGA TAATCTCTGGTATGAATATGAGCC
6320	Table 1	Hs.342873	AW451293	6992069	RC3-HT0230-130100-014-g06 cDNA	-1	TGCTTGGGAAATTTGGTTTGTAAACC TAAAATAGCCCTTATTTCTGGGGA
6321	Table 1	Hs.342735	AW452096	6992953	UI-H-BI3-alo-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3068186 /clone_end=3'	-1	CTTTCTGCCTGAAGCTGCCCCCATGA CTCCCTTCTTTGTGCAAAAGCATG
6322	Table 1	Hs.80618	AW510795	7148873	hypothetical protein (FLJ20015), mRNA /cds=(31,522)	-1	ACCCAGTTTGTGCATAGTTCATGATC CTCTATAAAACCAGCTTTTGTGGA
6323	Table 1	Hs.259842	AW614193	7319379	cDNA FLJ11025 fis, clone PLACE1003968, moderately similar to 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT /cds=(159,1145)	-1	ACACCATTTCAGCGTTGGATCACAGA CAGCTCTTCCTTTATATCCCAGCA
6324	Table 1	Hs.334437		7793371	hypothetical protein MGC4248 (MGC4248), mRNA /cds=(70,720)	-1	TGGCATAATGTTGGATTGAATCTACA TTTTGGCAGAAGTTAAACATTCCC
6325	Table 1	Hs.151393	AW778854	7793457	glutamate-cystelne ligase, catalytic subunit (GCLC), mRNA /cds=(92,2005)	-1	AGAATGCCTGGTTTTCGTTTGCAATT TGCTTGTGTAAATCAGGTTGTAAA
	Table 1	Hs.120243		8361417	gamma-parvin (PARVG), mRNA /cds=(0,995)	-1	ATCGTTGGATTATCTTTGAACCCCCT TGTGTGGATCATTTTGAGCCGCCT
6327	Table 1	Hs.5734	BE218938	8906256	meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(395,3145)	-1	ATACAGGGTTCCATCCAGAAAGCATT CAGTCAGAGCAAGTTAAAGTCAGT
6328	Table 1	Hs.167988	BE222301	8909619	neural cell adhesion molecule 1 (NCAM1), mRNA /cds=(201,2747)	-1	AAGTTGTCCTGTGCTAAAGCAAGCGT GGGATGATCCTACCTACCTCTAGG
8329	Table 1	Hs.27774	BE348809	9260662	602386841F1 cDNA, 5' end /clone=IMAGE:4515730 /clone_end=5'	-1	AGCTAGTGATGTTTTGTCCAAAGGAA GATTCTGACAACAGCTTCAGCAGA
6330	Table 1	NA	BE348955		hs91h01.x1 NCI_CGAP_Kid13 cDNA clone IMAGE:3144625 3', mRNA sequence	-1	ACACAGACATATTGACCGCACACAAC ACTGAAATGGACTGACTTGAGAAA
6331	Table 1	Hs.56156	BE349148	9261087	601463367F1 cDNA, 5' end /clone=IMAGE:3866512 /clone_end=5'	-1	TGGTTCTCTGATTTGTAATGAGCACC TGGATATGTCAATTAAAATGCCCA
6332	Table 1	Hs.127428	BE466500	9512198	Homo saplens, Similar to homeo box A9, clone MGC:19648 IMAGE:2987818, mRNA, complete cds /cds=(62,880)	-1	GGCCTACTGACCAAATTGTTGTGTTG AGATGATATTTAACTTTTTGCCAA
8333	Table 1	Hs.122575	BE502246	9704654	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4 (EDG4), mRNA /cds=(6,1061)	-1	CGATAGAATTGAAGCAGTCCACGGG GAGGGGATGATACAAGGAGTAAACC
6334	Table 1	Hs.197766	BE502992	9705400	clone 23932 mRNA sequence /cds=UNKNOWN	-1	CTCAAACGAAATTGGGCAGGCCATTT GCGTGGTTTCTCTGGATAAGTTCC
6335	Table 1	Hs.61428	BE550944	9792636	602329933F1 cDNA, 5' end /clone=IMAGE:4431248 /clone_end=5'	-1	GCACATGACAGTAAGCGAGGTTTTGG GTAAATATAGATGAGGATGCCTAT
	Teble 1	Hs.122655	BE551867	9793559	hypothetical protein MGC14425 (MGC14425), mRNA /cds=(318,686)	-1	ACACAGGAACCGCTTACCCACCAGCT CTGCCCGCGTCTCTACCGCCATAG
	Table 1 Table 1	Hs.4310 Hs.341573	BE614297	9895894 9970781	eukaryotic translation initiation factor 1A (EIF1A), mRNA /cds=(207,641) tc38c11.x1 cDNA, 3' end	-1	ACAACTCAAGTGAAAAGATGTCTCCA GTTTCTGAAGATAACGCACGCTGA AAAACACTCCACCTAAAAGCAGGAAA
					/clone=IMAGE:2066900 /clone_end=3*		GATGGCAATTCTAAATAGCAGCTA
	Table 1	Hs.88845	BE674685		AV733781 cDNA, 5' end /clone=cdAASF08 /clone_end=5'	-1	CGCCGCTCCTGGAGACCTGATAACTT AGGCTTGAAATAATTGACTTGTCT
	Table 1	Hs.181015		10036595	signal transducer and activator of transcription 6, interleukin-4 induced (STAT6), mRNA /cds=(165,2708)	-1	ATCCCATTCTCCCTCTCAAGGCAGGG GTCATAGATCCTAAGCCATAAAAT
6341		Hs.108327	BF001438	10701713	(127kD) (DDB1), mRNA /cds=(109,3531)	-1	ACAGCATGAGAAACTGTTAGTACGCA TACCTCAGTTCAAACCTTTAGGGA
	Table 1	N A	BF056055		7k07h12.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3443950 3' similar to contains element L1 repetitive eleme	-1	CACAATGCTGCCTCCTCTGTGGATGA CTGATGGCAAGAGTCTGAATTGAA
	Table 1	Hs.43857	BF058599	10812495	mRNA for KIAA1247 protein, partial cds /cds=(285,2942)	-1	TAAGAAATCCCAATTTTCAGGAGTGG TGGTGTCAATAAACGCTCTGTGGC
6344	Table 1	Hs.144583	BF059133	10813029	Homo sapiens, clone IMAGE:3462401, mRNA, partial cds /cds=(0,153)	-1	CGGCAGGGTGGCCTGTAACAATTTCA GTTTTCGCAGAACATTCAGGTATT
6345	Table 1	Hs.144519	BF061421	10820331	T-cell leukemia/lymphoma 6 (TCL6), transcript variant TCL6a2, mRNA /cds=(1767,2192)	-1	GCTGGAGGGAGAGGCACTGGGGAAT TTTTCCTGGTGAATACTGAAGTTAC

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					Table 8		
6346	Table 1	Hs.96566	BF194880	11081165	602137338F1 cDNA, 5' end /clone=IMAGE:4274048 /clone_end=5'	-1	TGATACTTTGGTTCTCTTTCCTGCTCA GGTCCCTTCATTTGTACTTTGGA
6347	Table 1	Hs.111583	BF197608	11086855	602365742F1 cDNA, 5' end /clone=IMAGE:4473923 /clone_end=5'	-1	ACTGCCAGTGAAGACTGTAAAGACAG AACACACTATTTTGGAGGGAGGAT
6348	Table 2	NA	BF197762	11087169	7p91f02.x1 NCI_CGAP_Skn1 cDNA clone IMAGE:3653139 3', mRNA	-1	AGGAAGAGCCTGCACCTGTGGTGGA ACAATCAGGGAAAAGGAAGTCAAAA
6349	Table 2	Hs.50785	BF221780	11128957	sequence SEC22, vesicle trafficking protein (S. cerevisiae)-like 1 (SEC22L1), mRNA	-1	TTTGGAGCTTCTATAGGAGTGGAGAG GGGCAGCTCATTGTTGAGAGTTGC
6350	Table 1	Hs.250811	BF432643	11444806	/cds=(119,766) v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA /cds=(170,790)	-1	TGATCTGACTGGAAAACAATCCTGTA TCCCCTCCCAAAGAATCATGGGCT
6351	Table 1	Hs.293476	BF435621	11447923	hypothetical protein FKSG44	-1	CGTTTTCTGAGCATCCGTTGTGCCTT
6352	Table 1	Hs.174104	BF445405	11510543	(FKSG44), mRNA /cds=(126,1520) 601438710F1 cDNA, 5' end /clone=IMAGE:3923643 /clone_end=5'	-1	AACATTTTCTGCTTGTCCTTTGGG ACTGCTGTTGCATGAATAGATGATAC AAAGCAAGTGATGAGGTTGGTATG
6353	Table 1	Hs.295726	BF447885	11513023	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	-1	AGTGAAAACTGGTACAGTGTTCTGCT TGATTTACAACATGTAACTTGTGA
6354	Table 1	Hs.161311	BF478236	11549065	(ITGAV), mRNA /cds=(41,3187) asparaginyl-tRNA synthetase (NARS), mRNA /cds=(73,1719)	-1	TGTCCTCTGAACCTGAGTGAAGAAAT ATACTCTGTCCTTTGTACCTGCGT
6355	Table 1	Hs.179703	BF507849	11591147	tripartite motif protein 14 (TRIM14),	-1	CCATTTCCACTACATGCCTTTCCTAC
6356	Table 1	Hs.300870	BF513602	11598781	mRNA /cds=(10,1230) mRNA; cDNA DKFZp547M072 (from clone DKFZp547M072) /cds=UNKNOWN	-1	CITCCCTTCACAACCAATCAAGTG AATACAGATTCATTTTATTTAAGCGTC CGTGGCACCGACAGGGACCCCAG
6357	Table 1	Hs.283022	BF514341	11599520	recipient receptor expressed on myeloid cells 1 (TREM1), mRNA /cds=(47,751)	-1	GCCTCTTTTCCTGTATCACACAAGGG TCAGGGATGGTGGAGTAAAAGCTC
6358	Table 1	Hs.146065	BF591040	11683364	AL580165 cDNA	-1	CTGGGGCCGTAGCAAAAATCATGAAA
6359	Table 1	Hs.170577	BF725383	12041294	/clone=CS0DJ005YB18;(3-prime) 602574255F1 cDNA, 5' end /clone=IMAGE:4702644 /clone_end=5'	-1	AACACTTCAACGTGTCCTTTCAAT CAGACCTGTGGGCTGATTCCAGACT GAGAGTTGAAGTTTTGTGTGCATCA
6360	Table 1	Hs.104640	BF726114	12042025	HIV-1 inducer of short transcripts binding protein (FBI1), mRNA	-1	AAGGCAACCAACCACATTAGAAGTCT TGGCACTTTGTAACGGAACGG
6381	Table 1	Hs.296317	BF938959	12356279	/cds=(0,1754) mRNA for KIAA1789 protein, partial cds /cds=(3466,4899)	-1	GAAGTGACACTGACTGTATCTACCTC TCCTTTTCTTCATCAGGTGTTCCT
6362	Table 1	Hs.26136	BF940103	12357423	hypothetical protein MGC14156	-1	AATTCCAAAGGAGTGATGTTGGAATA
6363	Table 1	Hs.133372	BF940291	12357611	(MGC14156), mRNA /cds=(82,426) AF150127 cDNA /clone=CBCBGA01	-1	GTCCCTCTAAGGGAGAAATGCA AGCCCCTCCACCCCACC
6364	Table 1	Hs.304900	BF980139	12347354	602286147F1 cDNA, 5' end /clone=IMAGE:4373963 /clone_end=5'	-1	TACAATGTGTTATTAAAGACCCCT CCATCCTTGAGAAATGTGGGCACCAA GTCCATAATCTCCATAAATCCAAT
6365	Table 1	Hs.6258	BG054968	12512220	cDNA FLJ14737 fis, clone NT2RP3002273, weakly similar to SCD6 PROTEIN /cds=(77,1466)	-1	TATGAGTTTATGCGTTTTCCCAGCCC TCCGAATCACTGACTGGGGCGTTT
8366	Table 1	Hs.5122	BG058599	12525258	602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5'	-1	AGTTGGAGCTATCTGTGCAGCAGTTT CTCTACAGTTGTGCATAAATGTTT
6367	Table 2	Hs.89104	BG058739	12525527	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	CGTGGGAGGATGACAAAGAAGCATG AGTCACCCTGCTGGATAAACTTAGA
6368	Table 1	Hs.166982	BG149747	12661777	phosphatidylinositol glycan, class F (PIGF), mRNA /cds=(67,726)	-1	GTGGTTTGGTCAGCATACACACTTCT CATTTCATTTGATGTACACAGCCA
6369	Table 1	Hs.184456	BG230563	12725596	hypothetical protein (LOC51249), mRNA /cds=(0.611)	-1	GTGTGAAGTGACAGCCTTGTGTGTGA TGTTTTCTGCCTTCCCCAAGTTTG
6370	Table 1	Hs.3353	BG236015	12749862	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCTTTCCCGTCTTTCTTCCTCACCTA TGTAATTTCAGTAGTCTCTCAGC
6371	Table 1	Hs.83623	BG654774	13792183	nuclear receptor subfamily 1, group I, member 3 (NR1I3), mRNA /cds=(272,1318)	-1	TGTTTCGTAAATTAAATAGGTCTGGC CCAGAAGACCCACTCAATTGCCTT
6372	Table 1	Hs.109007	BG655723	13793132	602342214F1 cDNA, 5' end /clone=IMAGE:4452602 /clone_end=5'	-1	GTGGAAATCAGCACACAACCACAATG ACATTTAAGCACAGGATCATTATT
6373	Table 1	Hs.14453	BG744911	14055564	interferon consensus sequence binding protein 1 (ICSBP1), mRNA. /cds=(47,1327)	-1	AGAATGGCAGACCTGTTTGCTGAAGT GTTCATAAGATAACAATAGGCTTG
6374	Table 1	Hs.2730	BI084548	14502878	heterogeneous nuclear ribonucleoprotein L (HNRPL), mRNA /cds=(28,1704)	-1	TGGGGATTTTGTTTTTAAGTCATTTGGT TTGGGGAGGACCTTGTTTATTTT
6375	Table 1	Hs.296356	Bl085832	14504162	mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162) /cds=UNKNOWN	-1	TGGACAAACTGACAGGGACTGCTTTG AAAGACAGGTACTCAGTTGAGTAT
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					Table 8		
6376	Table 1	Hs.132911	N20190	1125145	MR2-OT0079-290500-007-b03 cDNA	-1	AAGCCTGTTTTTCACTCTAAAAATTCA AGAGGACACGCTAAGAACGATCA
6377	Table 1	Hs.334731	N58136	1202026	Homo sapiens, clone IMAGE:3448306, mRNA, partial cds /cds=(0,2353)	-1	AGGTTCCCTTTCAAATAAAGATAAAG AATTTGACTTGGGACACTGCCAGA
6378	Table 1	Hs.303018	N94511	1266820	zb80g04.s1 cDNA, 3' end /clone=IMAGE:309942 /clone_end=3'	-1	CTGTTCGAAAGTTGGAGACTGCCTGT ACCCAGGTTGATAGTCAATTGTTT
6379	Table 1	NA	W68708	1377588	zd35h04.s1 Soares_fetal_heart_NbHH19W cDNA clone IMAGE:342679 3', mRNA sequence	-1	AGCAGAGTTAAGTTTAAATTTCCATTC TCACTAGTTTGTGACCTTTGCCA
6380	Table 1	NA	W86427	1400194	zh61c11.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA done IMAGE:416564 3', mRNA sequence	-1	TGAGTATTGTTGTGGGGGGGGGTAT GTCTGTATATAAATCTGTGCAGCCA
6381	Table 3A	NA			36G5	1	CCCTTGCAGATACATGAGACAGGCA GGGGCTGGAGTCTTGTTCCATCCTG
6382	Table 3A	NA			36F11	1	GAGTAGTTGTCTTTCCTGGCACTAAC GTTGAGCTCGTGTACGCACTGAAG
6383	Table 1	NA			37G7	1	GAGTCCAATCTACACTCTAGTAGTGA AGACAGAAGAGTTGGCATACGAGT
6384	Table 1	NA			37G8	1	GGCTGAACTTACTCATTAAGCCACAT AACTTCGAGTCAAGTTCCAGTCCA
6385	Table 3A	Hs.197345			thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA /cds=(17,1846)	1	GCTCTCAAGCCTCCTCCAATAAAGCT CTATCGGGAAACAAATGAACCAGT
6388	Table 1	NA			40E4	1	AGGAATGCACACATTGCTCCAGGATC ACTGTGAGGATTAAAGGAGATGGT
8387	Table 3A	NA			41E9	1	AGTAACGGAACAGTTCCCAGTACTCC TGGTTCCTAGGTGAGCAGGTGATG
8388	Table 3A	Hs.169476			Homo sapiens, glyceraldehyde-3- phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313)	1	GGTGTGAACCATGAGAAGTTCGACAA CAGCCTCAAGATCATCAGCAATGA
6389	Table 3A	NA			47E5	1	GGAGGTGTATAGGCTGGGATTTGAAA AGGAAAATAATCAGCGTGGTGCCA
6390	Table 2	NA			47D11	1	CCTAGACACCTGCATCAGTCAAGGTC
6391	Table 1	NA			50A11	1	ATGGATATTGGGAAGACAGACAGC TCCAGCAGATATAGGAAGCAGTGTAT CTAAACAGACAAATAAAAAGGCCT
6392	Table 3A	Hs.132906			DNA sequence from clone RPH1- 44PH1 on chromosome 14(23.1-42-1. Contains the 6" end of the SLAM gene for signaling hymphocytic activation molecute, a SET (SET translocation (myeloid leukemia-associated) protein pseudopane, the CD48 gene for CD48 antigen (B-cell membrane protein), the gene for a novel LY8 (ymphocyte antigen 0) like protein and the 5" and of the control of the control of the control of the and GSSs (cds=(41,1048)).	1	ATCTACTOTACOGGACTTCAACTCAC GCAGTGAGACTGGTGGGGCACGGG
6393	Table 1	NA			52B9	1	TGGTTTAATGGAAAATGCTCTGGAAA ATTCTTTTGCAACAGTTCATCGCT
6394	Table 1	NA			53B1	1	CACTAAAAGAGTGGGGAGGTGCAGC ACCTGGCTGGGGAACAAGAATATGG
6395	Table 1	NA			53E3	1	AAACGAATCACGTGCCTCGAAAGGG ACATATATTGTTCCTTTAAGCATTT
6396	Table 1	NA			53E10	1	AAGGGTTCAATTTCTTCTTTGGAAGG TGATGGTAAGGGTGTGGCTCCAGA
6397	Table 2	NA			53G7	1	TGGACAATTCCAAGTCCAAGAGGACT GTCTACTTTCGACCTTGTGTGATT
6398	Table 1	NA			54F4	1	TTGTGTTAACCTGTTGTCCACGCTAA GATACAAACTTCCCGGAGGAAAGT
6399	Table 1	NA			54G9	1	TGTCACAGTGTTCTATTATTTGCCCG GTTCTTAAAGTGAGAGCATCCTGA
6400	Table 1	NA			59G1	1	ACAATGATATTGATGAGGCACCCAGT CTTTTCATTTACTCTGAGTGAAGT
6401	Table 1	Hs.48320			mRNA for ring-IBR-ring domain containing protein Dorfin, complete cds /cds=(317,2833)	1	AGATCGAGATCTTCAGTCCTCTGCTT CATCTGTGAGCTTGCCTTCAGTCA
6402	Table 1	NA			60G8	1	GGCCAGAGACCCTAAGCTGCTTAATA
6403	Table 2	NA			62C9	1	CATTTATACCACATCCTTCTCAGC CCCTTGGAATTACTTGTTCAACTTCTT TCTTTCCCACTAGACGGGGACTT
6404	Table 3A	NA			62F11	1	CTTTGTAGATGCAGAGAGAAGCTATA
6405	Table 1	NA			63E1	1	AGAAACCCCAGTACTTGCCGGGCG ACTGCCACATCTGACTTTACAGAATA ACCAATGTAAGTTAAAATAGAGAAAC AG
					536		

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			Table 8		
6406	Table 2	NA	65B1	1 AGTCTTGCGAGTCAACTCAGAC	TCAA
	Table 2	NA NA	65D10	ATGTAGAACTGGGAAGGACAGT 1 AGCACTGTGCAGATGGCTTTAG	rgc
	Table 2	NA .	65D11	TTCAGAACAGAAGCACAATCTG AGCACTGTGCAGATGGCTTTGG	TT
	Table 2	NA .	65D12	TTCAGAACAGAAGCACAATCTG 1 CTATGGAGTCTTGGAGGACACT	TT
	Table 1	NA .	6809	GTCACCATGCTAACACTGTGCA CCCTGTCACCCTTCGTGGCCAC	GAT
		NA NA	69F8	CAGACAGTAACTAGTGGATGCT	'AAA
6411	Table 1	NA	9918	1 GAGAGAATAGGGTAGAGAGAC ACTTGGGTAGAGATGACCGGG	ATTC
6412	Table 1	NA	69H11	1 AGTGGAAGCTAGGAGAAATATC GTGTTAGGGACTTTGAAGTTAC	
	Table 3A	NA	70B6	1 CTGCATCTCTCTTTACTACCAG ACAAAGTGGGGTTTGGTGGGA	3T
6414	Table 3A	Hs.17109	integral membrane protein 2A (ITM2A), mRNA /cds=(139,930)	1 TCTCTGACTTCTTATTACCAAGC CTCTATCTGTTGCCTCTTACTC	SACA
6415	Table 2	NA	72D4	1 CAGTTCCCAGATGTGCGTGTTG CCCCAAGTATCACCTTCCAATT	TGGT
6416	Table 3A	Hs.234279	microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA /cds=(64,670)	1 AACGACCCTGTATTGCAGAAGA AGACATTCTGTATGCCACAGAT	TTGT
6417	Table 2	NA	72D8	1 GGGTCCCGAGCCCTTCAAGAG ATTTACTCAAGTTTGTTCCCTTG	
6416	Table 1	NA	73C4	1 CACTGAAGCCAAACCACAGAAC TTGAGAATGAGGAGACAAATGA	
6419	Table 1	NA	73H4	1 AGGTGAAAATTACTCTTCAGAA GCAGAGTGGATAATGGCCCATC	
6420	Table 2	NA	73A7	1 TGCAGTGAGACTACATTTCTGT AGAAGATGTGTGAGTTCCGTCC	CTAA
6421	Table 3A	Hs.174228	small inducible cytokine subfamily C, member 2 (SCYC2), mRNA /cds=(0,344)	1 TCCAGCCAGCCAGCTCATTTCA ACACCCTCATGGACTGGGATTA	CTTT
6422	Table 3A	Hs.3945	CGI-107 protein (LOC51012), mRNA /cds=(84,719)	1 TTTCATACATTGGAACTCCACC TTTGGACCAACCCCAGAACAGA	TGAC AGC
6423	Table 1	NA	75A2	1 AGCACCGGAATACAAAATGAT TGCTGCCCTCCTAGATCTCAGG	ACTA GA
6424	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222)	TGCCCATACACATGAGTATTTG AAACATGTCTTCTTTGTAGCAG	TCTA CT
6425	Table 2	NA	75B12	1 GCAAATCTAAACTGCAGGAAAA TGCACCCGAAGTATTCAGATCC	CT
6428	Table 2	Hs.205442	601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5'	1 GGCCCAGTGCTAATGTAACCAA GCCATGTCGATATTGGAAACCA	ΝTΑ
6427	Table 3A	NA	101G7	1 GGGGAAGAACAAGATAATCTAC CTCACCACAGTCTATGCCCAGC	STGAC SCC
6428	Table 3A	Hs.179585	minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA /cds=(44,2470)	1 AATTCAACTGAAGGCGAGGAAT GTGATGAAGCTGAGATCAGGA	
6429	Table 1	Hs.119640	hBKLF for basic kruppel like factor (LOC51274), mRNA /cds=(55,1092)	1 CACCTATATCGAAAGTTTGGGC CTCCCATTGGTGGCAAAGACC*	
6430	Table 3A	Hs.215595	guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA/cds=(280,1302)	1 TGGTGGAAAAGTGTGTCTGTCT ATTACACTCAAGTTTACCTCTG	GACA
6431	Table 1	NA	105A10	1 ACGATAATACTGTTGGTTACTG AAATATTGGAAGCTAATGTAAA	CCAT ATGC
6432	Table 1	NA	107G11	1 TTCTCTTATAAAGGACAGCAAG AATGGAGCAAGGAGCATTGGA	TTTAA
6433	Table 1	NA	107H8	1 TGGCCAAAGAATAGAAGCTCTA TTCCTTATTTCTATCGTGAAAAG	GACC
6434	Table 3A	Hs.64239	DNA sequence from clone RP5- 1174N9 on chromosome [p34,1-35.3. Contains the gene for a novel protein with IBR domain, a (pseudo?) gene for a novel protein similar to MT1E (metallothionein 1E (functional)), ESTs,	1 ACATGACCTGTGCAGTGTGTGG GAATTCTGTTGGCTTTGTATGA	
			STSs, GSSs and two putative CpG islands /cds=(0,2195)		
6435	Table 1	NA	109H9	1 TGACATAACTACCATCCCTGCA ATGAACCCACCCTCACAGCTTC	ACTA
6436	Table 3A	Hs.80261	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related) (HEF1), mRNA /cds=(163,2667)	1 GAATGACATAAACCCCCTCCGG AGGTCCGGCCTTCCAGCTTGTG	STCTG
6437	Table 3A	Hs.1422	Gardner-Rasheed feline sarcoma viral (v-gr) oncogene homolog (FGR), mRNA /cds=(147,1736)	1 GCCTTTCTCACTCCATCCCCAC AGTGCTCAGACCTTGTCTAGTT	

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6438	Table 3A	Hs,333114	AV713318 cDNA, 5' end /clone=DCAAAC09 /clone_end=5'	1 TCGTTTTACAACGTCGTGACTGGGAA AACCCTGGCGTTACCCAACTTAAT
6439	Table 1	NA	129A12	1 TGTTTTGTTTTCTGAAACGAAATCCTG CTCTGTTGGCCCAGCTAGAACGC
6440	Table 1	NA	129F10	1 CAGAAGCTGGATGACGTTGCTCCATC TTCACTCTGTTAATGAGACATGAT
6441	Table 3A	NA	137D4	1 CACATCTTCCATTCAGCCCTACCATG AAAACCGTACCTCGGGCGCGACCA
6442	Table 1	NA	142F9	1 AATTTGCTTTAAATTGAGTTTCCTTGC CATTGCACACTCCTATCTTTCTG
6443	Table 3A	Hs.250655	prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(155,487)	1 CAGATGACACGCGCTCTCCACCACC CAACCCAAACCATGAGAATTTGCAA
6444	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript varient 2, mRNA /cds=(104,1222)	1 CCCATGCTGTTGATTGCTAAATGTAA CAGTCTGATCGTGACGCTGAATAA
6445	Table 1	NA	149G2	1 GACACAGACAGACCAAGCTATAGTCA GACCTGGTTACACACATACACACA
6446	Table 1	NA	149A11	1 TGGCAAAGATCACTGAAATTTAGGAC ACCAAAGCTAAAACCCCAAATGCT
6447	Table 3A	NA	151F11	1 GCTTGTGCTCGAGACCGCTTGCTATA GAAACGCTGAGCTGCTGGTTTATG
6448	Table 1	NA	162E8	1 CTGGTTAAAAGCCCCATTACTGACCT TCGCCGCCACCACGCCTATCACTA
6449	Table 3A	Hs.334330	calmodulin 3 (phosphorylase kinase, delta) (CALM3), mRNA /cds=(123,581)	1 GCATCCACCTCCTTCTCTGTCTCATG TGTGCTCTTCTTTCTACAGTA
6450	Table 1	NA -	170F7	1 TTAAATCTATCAAGAATTCATCCAAAT TGGTACCCTGCCGGGCCGCCTCG
6451	Table 2	NA	170F9	1 AGTGCTGTATTGACTTTGCTCGGCAG TAGATGAAGCTATTCTGAACCCAA
6452	Table 3A	NA	177A3	1 TGCTGGACAAAGACAATGAGATGATT ATTGGTGGTGGGATGGCTGTTACC
6453	Table 1	NA	331A3	1 GTGGAAAAGTCACTACCAGGCTGGC AGGGAATGGGGCAATCTATTCATAC
6454	Table 1	NA	331A5	1 AAGGGACAGGGAGCGGCACAAAAT AAAACTTAGTTTGGTAGAAATTATA
6455	Table 3A	NA	146C3	1 TCAAAGCACTGGAGATGAGAGCCAG GATGGACCCGAAAAGAATTTTACAG
6456	Table 1	NA	146D8	CAGGAACATGGCTGCAGCATATAAAA AGAATTGAATTCCATACTTTTGTTAAC CCT
6457	Table 3A	Hs.153	ribosomal protein L7 (RPL7), mRNA /cds=(10,756)	1 TTGCCATAACCACGCTTGTAGATTAG TTCATTTACTGACTTCAGATTGGG
6458	Table 1	NA	158G6	1 TTACAGGCAACCGGAGCATCCAATCA CCTTTCTCTAAGAGAGTACCTCGG
6459	Table 1	NA	158H6	1 AAAAGCATCTTCGAGAGGGACTGTCA ATTCTCGACTATTTTCCAACCCGC
6460	Table 3A	Hs.119598	ribosomal protein L3 (RPL3), mRNA /cds=(6,1217)	1 AAGAAGGAGCTTAATGCCAGGAACA GATTTTGCAGTTGGTGGGGTCTCAA
6461	Table 1	NA	158E9	1 AGAGACACCTAAATTACAGATTTGTG AGCTGAGAGCTGGAGTTTTTCATT
6462	Table 3A	Hs.326249	ribosomal protein L22 (RPL22), mRNA /cds=(51,437)	1 AACAGCAAAGAGAGTTACGAATTACG TTACTTCCAGATTAACCAGGACGA
6463	Table 3A	Hs.297753	vimentin (VIM), mRNA /cds=(122,1522)	1 AGCGCAAGATAGATTTGGAATAGGAA TAAGCTCTAGTTCTTAACAACCGA
6464	Table 3A	NA	155H10	1 GCATGGACAAGATGCCAAGGCCCGG ATGCTTTAGGATGAAGTTCTTATCT
6465	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	1 CCTCCAGTCACCATACACAGGTTACC AGTGTCGAACTTGATGAAATCAGT
6466	Table 1	NA	159F6	1 CCAAACATCTGGACTTGTGACTGTAA AAGGGGAGGAGGTAGCCAATGATT
6467	Table 3A	NA	166F3	1 TTATGGTGGTCGGGGTGGGTAG TTCAATGGGAGGTATGGGATTTATT
6468	Table 1	NA	166F6	1 AGCTGTCTGGCTCAAAGATCTACATT CTGAAGTTGGCTGGAAATGTCTTG
6469	Table 1	Hs.8121	Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427)	1 CTGGTTCCTACCAGTGCCAGTGCCTT CAGGGCTTCACAGGCCAGTACCTC
6470	Table 2	Hs.25130	cDNA FLJ14923 fis, clone PLACE1008244, weakly similar to VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 /cds=UNKNOWN	1 TGACACAGACTGTTTCAATCTTGGAG CAGCGACTGACTTTGACAGAAGAT
6471	Table 1	NA	168A9	1 TGCTATTTAAAGCACCATGATAAATAT GAGGCCACTTGGAAATCCATCCA
6472	Table 1	NA	171F11	1 GCAGGCGATGCTCTATAATCTAAAAT GTATCTCTCTTTCCCTAAGCTGAA
6473	Table 3A	NA	171G11	1 AAGTAAGACCACCTGTGAACTTGATC ATTATCTGGCGCACATAGGAAGAT
6474	Table 1	NA	175D1	1 GCTGGGGCTGGGAATTGCGTGGGCT AATGTGTCATTTGACTTAAGAAACT
6475	Table 1	NA	182H1	1 TTTGGGAAGAACCGATTGCTAAATTA TGCCTAATTCATGTCAGAAGAGGG
			538	

			Table 8		
6476	Table 3A	NA	184B5		GCAGTATACCATTTATATAGCAAA
6477	Table 3A	NA	184D2	1 CT	GCCAGTGGCCAGTTCACTGTAT GCCCTTTGGTAGTGAGAGGACCA
6478	Table 1	NA	184H1	1 C/	SCCAATGATGCTTTTAAGTAACCT ATTTCTTCATCTCTAAGGCACACTT
6479	Table 1	NA	46D1	1 G(CTACCCCTCTTTGCTGACCCCAG CCTGCGTGTCTGTCTCAGTGTTTCC
6480	Table 1	NA	98C1	1 AA	GTCCTCCTCTAAGTACTCTAAA
6481	Table 1	NA.	98C3	1 AC	CCATGAAGGTAGTTTTCAAACA CAATAGAGAAGAAGCTCTAGAAGA
	Table 2	Hs.205442	601439689F1 cDNA, 5' end	CA	MAAATCCCAAACCTTGGCACAAA GCTTCAACAGAAACATCAAATGCCA
0402	Table 2	118.200472	/clone=IMAGE:3924407 /clone_end=5'		BACCAGTGAGAGAGCGTCAAAAA
6483	Table 1	NA	98H4		CAAGCCCACTAAAATAAACATCTAA CAGCATCTTTCCCCCCATTATAGG
6484	Table 1	Hs.169363	GLE1 (yeast homolog)-like, RNA export mediator (GLE1L), mRNA /cds=(87,2066)	1 A7	GGATCTGTTCCTCTGTGCTAAATG TTGTGGCAGGGTGTGTTTGTGG
6485	Table 3A	NA	113F12	1 G0	CGTAATGTCTCGGGATCTCTAATA
6486	Table 1	Hs.30212	thyroid receptor interacting protein 15 (TRIP15), mRNA /cds=(15,1346)	1 AC	GGCACTCCTCAACCAGTGTTCACTG
6487	Table 3A	NA	173A10	1 AC	BAGAGGGTTTTAAGGGAGGGCTTG BAATACTTGGGAGAATACGGAAGG
6488	Table 3A	Hs.334853	hypothetical protein FLJ23544 (FLJ23544), mRNA /cds=(125,517)	1 A7	GAATTTGAAGACATGGTGGCTGAA AGCGGCTCATCCCAGATGGCTGT
6489	Table 3A	Hs.20252	(FL223-4), ill. (FL23-4); ill. (FL23	1 T	CCACAGATAGGTAAGCCAGGCGC GCAAGATGAGACTGTATTCAGTTA
6490	Table 1	NA	174D1		CTTGTCCTAGTCATTGTGGCAACCC
6491	Table 1	NA	45B9	1 T	CTGGCAAGCTCTTGTCATGGTGTT BACACTTCCTTCTGTCTTCTTGG
6492	Table 1	NA	45H8	1 T	TCAACATGCTTGTGTGTTTGG TCAACATGCTAGATCCATCAGAA CTGAAGGCGGGGAGAAAGCTCTC
6493	Table 1	NA	111H6	1 G	STACTCAAAGGAAATTACTCTTTCT FGGAACCCTGGCAGAAAGTTTTA
6494	Table 1	NA	111E12	1 A7	TGGTACCTGGCAGAAGTTTA TGGTACCTGGCCCGGCGAGCG
6495	Table 1	NA	111H11	1 A7	TTAAGGTTTTTTAACATCTACTTTGGG BATGGAGCCTTCAATGAAGTCA
8496	Table 1	NA	112H3	1 G/	AAAGACTACGAATTTCGCTGGGAG FAATAGGGAAGCCTTCCACATAAA
6497	Table 1	NA	112E9	1 A/	ATGAGGTCAGCAATAACCTTGATT GGTCCTCCACTGGCAACATTTTA
6498	Table 1	NA ·	114G3	1 C	TCTCTCCCTGTAACCAGGCAGTGT
8499	Table 1	. NA	117H6	1 G	TTGCCCTGATCTGGAAATCCTGTTG FTCTTCTGGGATGAAGGAACCTC
6500	Table 1	NA	165E7	1 T/	AGATAACCCACAGGCACTTCCTGT
6501	Table 1	NA	165E11	1 A7	TGGGAACAGGATGTTAAATACACAC
6502	Table 1	NA	165F7	1 C	CTCTGCTATCACTAGAGAATGTAGA AATGGAAATGGCTGCCTTTATGC
6503	Table 1	NA	176A6	1 G/	ATACAGATGTGATTATTCAGCCTCA GGGGACTTCTCCATTGCGTAACG
6504	Table 1	NA .	176G2	1 TI	TATTGTTACCAATTAGAATCAGCAAT CAACTGTGCGGTGATTTGGCCT
6505	Table 1	NA	176E10	1 TO	CATCACTTGGGTTAACTAAAGGTTT CGTATCACACAATTACACTACAA
6506	Table 3A	NA ·	176F11	1 TI	CATAGTCAAACAAAAGGTAAGATC FGCATATACCCACGGCAACAAGG
6507	Table 1	Hs.232400	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA	1 C	CCACCCCTTCCCCTCCATGTGAAG
6508	Table 1	NA	/cds=(169,1230) 71F2		GGAGACATGCTGATTCCACTCAAAG
6509	Table 1	Hs.172028	a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715)	1 A/	ICTCATAATAAACAGCTTTGGCC AATAAATTTGGAATGGGACATTGTG IGTTTCACCTTCAATGCTGTTAA

			Table 8		
6510	Table 1	Hs.180610	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein- associated) (SFPQ), mRNA	1	AGAACAGTCTTGGGTTCAGGGGTGT GATGCCAGAATGTATTTTCGTACCT
6511	Table 1	NA	/cds=(85,2208) 124G4	1	AAGGCGAAGTCAATCCCATCTCCCTG
6512	Table 1	NA	124C8	1	AACCCAACTGCCAGTAGGTAGTTC AGTTAAACTGTTGGTGAGGTAGTGTG
6513	Table 1	NA	124F9	1	TCAGGTACTCTGTATATTAGCTCT ACTGGATAAACAGAACGGATCAAAGA
6514	Table 3A	NA	127A12	1	TAAAAGTATTCTTGTTGCCTGGGC GTCCCTTAGGGGAGGGAGAGTTGTC CTCTTTGCCCACAGTCTACCCTCAG
6515	Table 1	Hs.50180	601652275F1 cDNA, 5' end /clone=IMAGE:3935610 /clone_end=5'	1	ACTGGACTACTGAACTTTAGAATACT GTCCTAAGGAAATAGGTCTGGGCA
6516	Table 1	NA	161E8	1	CAAACAACAAAAGTGGCCTCCATCGC TGTGAGCCTCTCAAGGGACAGGGC
6517	Table 1	NA	186E8	1	AAGGTGGCTGGCTTTTATGATACAGT GGTGGTAATGTAGCCCTTTTTGGT
6518	Table 2	NA	191F6	1	TGCTCAATTGCCATACATGCACTATA GGCCGGGATAGAAAATCGTCAGCT
6519	Table 3A	NA	193G3	1	TTCAAGGATGTGACTGATATCTGGTG TGGTTTATTTTGTTTGTTTTGGGG
6520	Table 1	NA	194C2	1	AGCTTTGGAAATTTGAACAAGGTGGG GACAAAATCAGGCAATAACAGACT
6521	db mining	NA	458C6	1	CACTTCCTGAGTGTTTCCTGAGAACA AAGGATCAGAGCTTCGGCTGTGAG
6522	Table 1	NA	458E4	1	TTTTCCTTTTCGCTGACTTTCCCACTC ACTGTCTGTCTCTCATTTTCTCT
6523	Table 1 .	NA	458G10	1	GCATGGGAATTGGCTGTCATCACTCA TAGCACGGTGTATAAACTCAAGGA
6524	Table 1	NA	459B3	1	GTCCACTCAAGTTACCTGGCTGTCTA TCTTTTGGCTGACCCCTGAAGCGA
6525	Table 1	NA	459D2	1	CTAAGTAAGCAAAGAGGCAGAGGGG AGGAGGGGAGTGTTTGGTACTGTCC
6526	Table 1	NA	459E6	1	TGGTGCGGTGTTCATGATTATTATGC AGGGTGGAAGTTCAGTATTTTGGTC
6527	Table 3A	Hs.20830	DNA sequence from cosmid ICK07210 on chromosome 5. Contains a 800 s. Ribosomal Protein L38A LIKE s. Ribosomal R38A L38A L38A L38A L38A L38A L38A L38A L	1	AGCACATTTGTGCAGAAAGGTTTTGC AGGTATCTGAGGCACTGCTCACCT
6528	Table 3A	NA	460D5	1	AGAACAACACGGGATTGAAGTGGGA AGAGATGGGACCCTCATTGGATCTG
6529	Table 1	NA	460B9	1	GGAACAATAGACCTCTTCACTAGCTC CCTGCTGTTTGATGGTTTGGTT
6530	Table 3A	NA	461A4	1	AGAGGATGACTTTGAGGTAAATGTTT ACGATGCACGGTTTTAGGCGATGT
6531	Table 1	NA	461G6	1	GTGTCCTGGGGAGTGAGGAGAGGTG GAGTAGACTCTGAGAGGAGTGAAAA
6532	Table 1	NA	461D9	1	AGATCATGTCTGGATTGTGTTTCCTA TTACCTAGAGACGAACACAGATCT
6533	Table 3A	Hs.80768	chloride channel 7 (CLCN7), mRNA /cds=(38,2455)	1	GTGTCCCAGGACGAGCGGGAGTGCA CCATGGACCTCTCCGAGTTCATGAA
6534	Table 1	NA	461H7	1	TGTATGGCTTATAGCCAGAGATGAAA CAGAACCCAAGTTAATATTGCCAG
6535	Table 1	Hs.333513 .	small inducible cytokine subfamily E, member 1 (endothelial monocyte- activating) (SCYE1), mRNA /cds=(49,987)	1	AGGTTTCAGAATCTGGGCCTTACCTT TACAGGTTCAACAAAAGAATGGCA
6536	Table 1	NA	463A5	1	AAGATGAGGCGTAGCTCATGTACAAA TGCAGCATTCTCATAAGTGCTTTA
6537	Table 1	NA	463B2	1	AGATAGTGGTATTTGGGTGCTGGGCT TGTCTGAACTGAGGAGGTGGGTGC
			540		

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6538	Table 1	NA	463C5	1	CCTTGCACCAGAGACGACTGACATAT
6539	Table 3A	Hs.40919	hypothetical protein FLJ14511	1	ATAGATGGGAGTCACTCATGCGCT GGTGTAGCGTGAAGATCTGGACAGC
			(FLJ14511), mRNA /cds=(22,1272)		GCACTACGACCCGGGCCACTGTTTC
6540	Table 1	NA	463H5	1	AGAAGCAAACCTGTGAAGCTACTATC GTTTATCATCAGTGTGAATGCACT
6541	Table 1	NA	463A7	1	TAGTGATACAATTTGGGGTGCCAGAG
			100010		GTTGGGGGTAAGGAATTTTGAAGC
6542	Table 1	NA	463B10	1	GTGTGGCCTAAGGAACACCTCTTGTG GGGAGTAAGAGCCAGCCCTTCCTC
6543	Table 1	NA	463C7	1	AGATGCGGGCGCAAGCTTATGTCCT
6544	Table 1	NA	463F10	1	GTTATGAGGGTTTAAATTAGATTGG TCATAACGCCCTTCAAAACATTGAAT
					AAAATCAGTGCAAAACATTGAGCA
6545	Table 1	NA	464C2	1	TGAGAAAGGAGTTAGCAGAATATTAA CATACCGAGAAGCTGTTGTTAGCA
6546	Table 1	NA	464C5	1	CTGGAGACTCAGGTCGCTTAAGTGG
6547	Table 1	NA	464C10 .	1	AGGGACGGGCACAGCCATTCCTCC AAAGACCTGCCACTTATTTTTTGGCTC
					TCATCTGTACTCTTAAGTGTGTGT
6548	Table 1	NA	464D8	1	AGACACAGCTGCAGAAAACTTATTCT TTTCAAGCATGCACAGTCACAAAA
6549	Table 1	Hs.221695	7k30d01.x1 cDNA, 3' end	1	CATTCAACAACACAAACCGAGCACCT
			/clone=IMAGE:3476785 /clone_end=31		ACTGTGTGCCACGCCACAGACAAG
6550	Table 1	NA	464E7	1	CCTAGGAAACACAGGTCAAAGAAACA
6551	Table 1	NA	464H12	1	CAGTCCAACATGTATTCAGAATTC AAACGCAATCTATTTTAGGTTTGAGAT
0001		NA .			TAGAAGCTGAGGCCAAGGACTCA
6552	Table 2	NA	465B3	1	TCCTCCAGATGCATGGTCCGTGAAGA AATTTAATAGCAAAGACGAGAAGA
6553	Table 1	NA	465G2	1	GGCTCTCATGCTTATGCCACACATCC
			465H5	1	TTGATTCTGCTTAGGAGTCTCTGG AAGCCTGAGCTAACAAGAGCTGAGG
6554	Table 1	NA	46500		ACAGTAGCTTATTCCTCTTTATGGG
6555	Table 1	NA	465A12	1	TGGATGATGGGATTGGATAAGCATGT
6556	Table 1	NA	465F7	1	GGACTGGATTGTGTTACAAACTCT TGCTGTTTCTAGGATTAACACGAAAT
			485GR	1	CATCACTTTGCCATATTTTGAGCT GGCTCAGCACAAAAGAGAATTCGTAG
6557	Table 1	NA	400G8	'	CACTTTCATGTGAAAGCAGACCCA
6558	Table 1	NA	465H10	1	GATATTAAGGTACTTTCAGTACAAATC TGGTGCTGTGAGTGGGCTCATCC
6559	Table 3A	Hs.136309	DNA sequence from clone RP4-	1	TCCAGTTTCTCATAAACAAATTCTTCT
			612B15 on chromosome 1p22.2-31.1.		ATCCTGGCATTTGGATTTGGGTT
			Contains the (possibly pseudo) gene for a novel protein similar to 60S ribosomal		
			protein L17 (RPL17), the gene for CGI-		
			 endophilin B1 and KIAA0491, ESTs, STSs, GSSs and two CpG islands 		
			/cds=(1011,1406)		
6560	Table 1	NA	515C12	1	TCATGGTCATAGCTGTAACCTGTGTG AAATAGTAATCAGATCAAAAAGCG
6561	Table 1	NA	515H10	1	ATATGTACCTGGAGGGCGGACGATC
6562	Table 1	NA	55G3	1	GAAATTACTAGTGAATTAGCGGCAG TGCGAGTGTAATTTCTGTAAGGAGGG
					TATGGGATAATTAATAGCACGCCT
6563	Table 1	NA	55F9	1	GCCCCAGCATTCAATTCATTTTGTA CCCTTAGTTTAAAGAACTTCTCCC
6564	Table 3A	NA	99E7	1	AACTTTGCTTTCTGAAGGTTTTTGGTG
6565	Table 1	Hs.319825	602021477F1 cDNA, 5' end	1	TACCTCGGGCGCGAACACGCTAAT ATTGACTCCACTTTGTGCCAAGCTCT
0000	TODIO -	110.010020	/done=IMAGE:4156915 /clone_end=5'		GCGGGTAGGCATATTTCATATCTT
6566	Table 1	Hs.17481	mRNA; cDNA DKFZp434G2415 (from	1	CAGTGGAGAAGCTGCACTGTCTCCG
0000	TODIC T	113.17401	clone DKFZp434G2415)	•	GGCTTGTGTGATCCGATCTCTGTAC
6567	Table 1	NA	/cds=UNKNOWN 116C9	1	AGCTTTGAAAGTAATGTCTAACCCTG
					CTGTCAGTTTATCACAAGTGCATT
6568	Table 1	NA	128F5	1	AGCTTAATTGAATTGGAGGAGCACCG AACAGGCAGTTTCCTGAGCAGTGG
6569	Table 1	NA	135F10	1	GCTCTCACTGATCTCTCTTCTCTATCT
6570	Table 1	NA	189F3	1	CTTTCTGCAGTTATACCAGCACT TGAGAAGAGCTGTGAAGGCAGAGGC
0010	I OIUIG I	110	100, 0	1	GGGCAAGTGCAAAGGTCCTGACTT
6571	Table 1	NA	189A8	1	AACTCCCTGTTCAGTTCAGTTGCTAA
, .					TGATCTCAAGCTCTTCCCTGATTA
6572	Table 1	NA	195H12	1	CAGCCTAATGCCTAACCACACAGATA CCATTGGTGGGCGACGTGACCCAG
					SOM TO

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			Table 8	
6573	Table 1	Hs.292457	Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds	1 CACCATCTTTTGCTCGGATACTAGCC CGCAATACCCACTCACCTACCACC
6574	Table 3A	NA	/cds=(498,635) 466C4	1 AGGGTCTCCACCTTACAGAAGTACAT GAACAACCAGAGATAGCAGGGCTG
6575	Table 1	NA	466D1	1 ACCAGGAAAAGTAAAAATCATAGTTG GTGTCTCTCGGGTTTCTCACCTTC
6576	Table 1	NA	466G2	1 ATGTATGAGAGAGATTCGAGATGAGT TAAAGGAGGGAAGGGA
6577	Table 1	NA	466H5	1 CATGAGTATTGGCACTGGGGTTCAAG TTCCAGGGCAGAGCAGGATAAGAG
6578	Table 1	NA	466B7	1 CTCCTGGGGCTGGAGTCCTGGTCTG CCTTCTGGGGACAGAGATTAGGTCG
6579	Table 2	NA	466B10	1 TGGAACTTCAGTCAAAAACATCTGTA CTTTGTACAGGACAAAGATTTGGC
6580	Table 1	NA	466C9	1 ATAGAACTTGTTTTACCTATGAGCCTT GCCTTGTATTTATTCACTGTGGC
6581	Table 1	Hs.7187	mRNA for KIAA1757 protein, partial cds /cds=(347,4576)	1 ACATCTCTTGTGAAAGTTCAAATGTTA CAGCAAGGTGTAAACACTCCACT
6582	Table 1	NA	121F1	1 GGGTGAATTAATCGGGAGATGGGTA GTCAGGGCAAATGATGGGTGGGTTT
6583	Table 1	NA	121A11	1 TGCAATTGTGGAGACAAATTGTTAGA GTTTAAATCCTGGCTCTGTTCCCT
6584	Table 3A	NA	121F8	1 GGACCTATGTCCTCAAGACATGGAAA CTACTAGTTCTGTCGTGCCAGGAG
	Table 1	NA .	178B2	1 AATTAAGGATGCCCTACCGACATCTA TCAGCATACCTGGAACAGGTTCGA
6586	Table 3A	NA	178B5	1 CGGCCAACCCAGGAGGGCAGGTGTT TTGGGCATCTGGTTTATAGTACCTC
6587	Table 1	NA	178F5	1 GCTGGGGTGAAAACTTGAAGACTCA GACCTCAGTGGAAACAGATGAATGT
6588	Table 1	NA	178C12	1 CCCCAGGCTCTGTGACGCTTGAAATT CTAATTAGCGCAGAAAAGGGCTAA
6589	Table 1	NA	462A11	1 CCTGACTACGTGTTTTCCCCACAGAC ATCACACTGGTTCACCTCGTTGAA
6590	Table 1	Hs.13231	od15d12.s1 cDNA /clone=IMAGE:1368023	1 AATGGAAAGACACTTCTGTATACACT GGAAATCTCAGGAAATTTCTTTTTTCC
6591	Table 1	NA	462D9	1 GACAGTACAGTACCCTAAGAGCACTG AGGAGGGCCACCCCACGTGAACTC
6592	Table 1	NA	462E8	1 TTTCCTTGGAGATTTCAGGCATCTTA GGCCGGAAGGGACCTCGAAGGTGG
6593	Table 1	NA	462F9	1 CTCCGCTTCTTTCACTCATTCGTTTAG TGTTTCTTTAAGCTTTGCCTTGT
6594	Table 1	NA	462F11	1 TCCACATTTTGATCATGCATTTATGAA AGCCCTGGGTTTGTTATTGAGAA
6595	Table 1	NA	462G12	1 GCTATCTTCTGCTGAATCAGCGTAAT GCTGATATACACCCTATTTTCTGT
6596	Table 1	NA	462H9	1 AAAAGAAAAGTTTTTCAACCCAGGGA ATTTATAGTGGGTGTCAGTCGAGA
6597	Table 1	NA	472B1	1 AGGAGACGATGTAGGGGGAAGTGTG TTAGATTGTAATGGAGGGGTTTGGA
6598	Table 1	NA	47201	1 GCTCTTTCCCAGACCCAGCCGCCAG GTTCTCTGTAGAAGAAAATAAATGC
6599	Table 1	NA	472E6	1 AAGGAGGAATGGGAATCTCAAGCTCA AGGGCACTCTCACTAATTGTGGGT
6600	Table 1	NA	472F4	1 AAATAGCCACCTTCTCCCCATTTTCT GTCAGAACACACACTTTATATCCA
6601	Table 1	NA	472G2	1 TTTGGTAAAAGAGATTGGAGGGGACA CCAGGGAAACCAGGATTTTCTGGC
6602	Table 1	NA	472D7	1 AAGTGCTAAGGCATTCTCTAAACTAT CTTTCCAGCTCCGGGCGACAATGG
6603	Table 1	NA	472G12	1 CCACTCTCTAAGTCAAGCGAGTCCTT CCTGCATACCTGTACTGGGTGCTG
6604	Table 1	Hs.75354	mRNA for KIAA0219 gene, partial cds /cds=(0,7239)	1 GGACTITGCAGGCTTCATTCCCTGTC TGTGTCTTTTCCTTCTGGTGTGTT
6605	Table 2	NA '	64G9	1 ATTTGCTGGCCAATCCTGCTGACTAT GAATCTTTGGGGGCACTGAGTTAC
6606	Table 1	NA	467E5	1 CTGGGGTACTGGGGAAAAGGAACTG GTATTGAGATTTTATATTTGGGGCG
6607	Table 1	NA	467A8	1 TTGAGTAAGGCTCAGAGTTGCAGATG AGGTGCAGAGAACATCCTGTGACT
6608	Table 1	NA .	467C9	1 GGTCACAGAGAGAAATGGTAGCTGA AGAAGCAGGGCACGAGGGCTCTAAC
6609	Table 3A	NA	467F8	1 TTTCCGGTATATTCGTGTGGGTTGAC TTTTTGTGTGTGTGTGTGTGTGTGGTGG
6610	Table 1	NA	468E6	1 GGATCTCTTGCTCCTCTCACCTGTGT GACAGACTACTAACAGCCCAACTG

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			Table 8		
6611	Table 1	NA	468B9	1	ACAGTGTGGGACAGAAGAGTGCTCA GTGATTAAATGCCTGATAATAGATT
6612	Table 1	NA	468E10	1	CTCTCTCGCAATTTACAACCGCTTTC AGTACCATTCACCGTCACTCCTCT
6613	Table 1	NA	468F10	1	CTTTGGGGAGTGGAGTTGTTGTAGAT GGGGAGAGAATCAGAACAAGGAGA
6614	Table 1	NA	468F11	1	CCTTACTGCTTACGGTCATCGGTCAT CAGCCCAACCCGCTTGGTTAGGTG
6615	Table 1	NA	468G12	1	AGAGTATAATTTCCCCAGTGTGGAGT GGTTAGTGTTGCTAAAGAAGAGGT
6616	Table 1	NA	468H11	1	CTGATGTCGTGTCTGCACTCACCTGG TCATGTGTTCTGTTGTGCGGTAGT
6617	Table 1	NA	469B6	1	AGGGGCAGAGAAGAATCCACACTCA CAAGAGATGACCAGGAGTAAAACTG
6618	Table 1	NA	469D2	1	CCCAGCAGAGGCCAACAAGCAGCCA TACCCAAACTTCAGCCAAAATAAAA
6619	Table 1	NA	469A10	1	TGTGCAAATACGGCGAGAAGAAGTG CATGAGAAAGTGCTTTATAAGCTGT
6620	Table 1	NA	469E12	1	CCAGCTTTTCCTTTGATGTTAGTTAG CAGTAAGTCACAGGTTTGAGCCCC
6621	Table 1	NA	469F8	1	GGCACGCATCCTCATTCCTGCATGCT CTTAGAATATCTATCAATGATCAT
6622	Table 1	NA	469G8	1	ACTTCTATACTCAGTGCGCTGTGGGT AACCAAGCAAGCAGGTTTGTTGTC
6623	Table 1	NA	470B2	1	GCGGGATGGTGGGAAGACAGACACT GCCTTAGAGCATGAATAATTGAAGA
6624	Table 1	Hs.118174	tetratricopeptide repeat domain 3 (TTC3), mRNA /cds=(2082,7460)	1	AGGTAGACTATTTAGCTGGAAGCATC CAAACAGGGGATTTTAAAAATACTCA
6625	Table 1	NA	470C3	1	AAAATGTAGGTTAAAACTCTCACTTAA GAAGGAGAAGATCTGAGTAAACCCA
6626	Table 1	NA	470D5	1	ACCTGAACAATGAATGAAGAAAGGAA GACTTGGTTCTTCTAGCTCTGGAC
6627	Table 1	NA	470E1	1	CATGGCTCACAAGCTCTAACACTCCC CTCCCTCCAGATCCTAAGAAGAAG
8626	Table 1	NA	470E5	1	TCTGAGCTTCACTTCAAGAACTGGTA GTCCAAAAGAACTGGTTCGTTCAG
6829	Table 1	NA	470F3	1	ACTTCACTCACTTTTTTAGCCTGTTCAT ATGAGCTTGTCAGTGCTTTTGTT
6630	Table 1	NA	470G6	1	TGAGGAGGATGGGAGGCGCACAGGC AATTTAGCTAGATATAGAAAGAGAA
8631	Table 1	NA	470B8	1	AGCTGATTTGGATTCTTGCGGTTTGC ATCGGTCTAATTTATCAAGTGTGT
6832	Table 1	NA	470G10	1	TCCATCCTTGGAAGCTTGACAAGCAT TCACACTACTGGCTCACCTACTAT
6833	Table 1	NA	471D6	1	TAGCACTGTAGCCAGAGTCCCTGCTT GTACCAGGAAGCTGGGTGGTTG
8634	Table 1	NA .	471F1	1	TGGATAGTCAGAATTACGTGTTTTGT GGATTGGGGAGGGAGGAAA
6635	Table 1	NA .	471F4	1	GCACTCCTGGAACCTTCTCACTAATT CGGGGACCAGTTTTGTGAATGTTG
6638	Table 1	NA ·	471F6	1	TTGCTGCGGATGACCTGACTGAGCC CTGGGAGACTGTGCTATAATCTCTC
6637	Table 1	NA	471E9	1	AGAAGGAGGATCTGTTCTAAACATCT GCGAGGGGAGGACAAAGCATTGAA
	Table 1	NA	471E11	1	CTTGCATCTGAGTGAAGATGAACCTT TCTTTCCCAGCCCTGAGAGAGAGGA
6639	Table 1	NA	471H11	1	GTCTAGCTGGCAGGTGATGGATGAAT GGATGAGCTGGCAGACCAACAGAA
6640	Table 1	NA	473E4	1	TGCATGGAAATGTTTCGAGTACGGGG AAAATAAGGGAGCCAAAACTGTGT
	Table 1	NA	473F3	1	TTTTAAGGTGTGACTCAATTTACAGG CATTCTGTATTTTTGCGATTTGGT
	Table 1	NA NA	473E11	1	ACCTTTGGGAGAAAGTCTTACAACTA CATGAAATGCAGATTTATGGACTC
6644	Table 1	NA NA	476C1 476D3	1	GAAGGGACAGAACAATCAACTGTGA GAGATGGGAAGAAAACTCAAATGGA
	Table 1	NA NA	476F5	1	CTAGTTTGGGGACTTTCATTGGGCAC GTGAATCCAGGAGGGCTGAATTTT
	Table 1	NA NA	476F5 476G3		GGCCCAGATTGTAGACAGCATAAAAA TAATTTTGGGCTTTTCCTGTTAAA
	Table 2	NA NA	476G3 478G4	1	CTGGGCTTCTTGTGTGAGAAGCACC GCAGCCAAGAACAACCAGTGCAACT
				1	GAAGGGGGATTCGGTGATGGGGGAA GCCAAGGGACAAGGGAAAAAGGAAA
	Table 1	NA	476A10	1	AACCCAACCATGAAAAAGAAGAAGCT CTGGACTACGGCCAGGCGTGGGAG
	Table 1	NA	476G8	1	TGGCTATTTGAGTTTTCTCTTACATGA AATGCCTGGCAACGTACACTGGC
6690	Table 1	NA	476H10	1	TGAACTCTGATTTCCGCCGAAACTAG GAGGAAACACCCAAAAGAAGACGG

			Table 8		
6651	Table 2	NA	477E1	1	TTTGCTGGGACTAAAATCAAAACTGC
6652	Table 1	NA	477E6	1	ACTGCAGAGCAGGTGAGGGTTCAT TGGAGAGTGTGTGTATTACCATTTTTT TACATTGCATCACATTTTACCATCTAT
					ATCT
6653	Table 2	NA	477A11	1	TTTGAAGCCCCTCATAGAGAAGAGAC TGTACCATAAGAGAAGCCCACTCA
6654	Table 1	NA	477D9	1 -	AACTCTCAGTCCATGAGCTTGATTAC TCCATTGTACCATTTGGAAGCCCA
6655	Table 1	NA	477D10	1	GTGGGTAGCCATTAAGTGGTCTGGC
6656	Table 2	NA	480A3	1	ACAGAAAGGGACAAGTAGCTTCAAG CTGGTGCTGAGTGGAGTCACAGTAA
6657	Table 1	NA	480B5	1	GGCTGTAGATGGAGCGCCCTGGGAA TTTTGATGTGACCAGTCGTGCATGGC
6658	Table 1	NA	480D2	1	GGGGGACAGGAGCTTAGGGGGAAT ATTATGCATGTCGAGGGGACAACTTT
6659	Table 1	NA .	480E2	1	TATTAAACAGGAGGGGTGTGTCTT TGGTCATGTTTCCCTCTTTACTCCAC
6660	Table 1	NA .	480E3	1	GACAGTTTCATTATTGTAACCAGG TTCTGTTGGTTATATGAATGGCAGTT
					ATTGTCTCCCAGTGTGTGGGTTCT
6661	Table 1	NA	480F3	1	AGTCCTGGCAACTTTACCTGGGAATT GTCTGTAATCTTTAAGCAGTGGCG
6662	Table 1	NA	480G4	1	AGGACTTATCTAGCTTTCACAGATTC AGAGTGCGTTTCAAACATCATTGT
6663	Table 1	NA	480C8	1	TTTAACAGGCTTATCTAGGACATAGG CCCAAGAGGGAGGAGGAAGGC
6664	Table 1	NA	460D9	1	CTCCAGGCCGAACGAGCCTCCACTC TGGATTAAGATCTGTCATCTTGACA
6665	Table 1	NA	480E7	1	GCAGGACTTGTGGCAGGACTCAACG GGAGAGAAAGAGGCTGAAACATAAA
6666	Table 1	NA	480E11	1	AAGAACATCCCAACTTTTCCGGTAGG
8867	Table 1	NA	480F8	1	CAAGTGTCAAGTCACCTGGACAAT TCTGTGGCTTGTTGTGGGACCCTGC
6668	Table 1	NA	467F11	1	GCCCTTTAAATTAGGGCATATTTTA GCGCTAAAAACCTGGTGATTAAATGA
6669	Table 3A	NA	499G1	1	CAAACAGAACGTGAGAAGAGATTT TCCTGCACACAACAAATAAAGACAAG
6670	Table 1	NA	518F10	1	AATAAAGGGCCACCCATCAGTAGC ATGTTGTTCAAATTAAACATCATACCA
6671	Table 3A	NA	524A12	1	CATGGGGCAGCTACCAATTTTT TAATATGAAAAGCTGGAAAAGAATTA
8872	Table 1	NA .	526B9	1	AGGGGTTGAGGAGACGTGCCGGGT GTTACCCTGACGAATGCAGTCCTCGT
6673	Table 1	NA	563B5	1	GTGGAATGTCTATGCCCTCTTGAG ACACCAGCAGTCATAGGGGAAAGGG
8874	Table 1	NA .	563D6	1	GAATACAGTTAATTGGGTATTTGTT ACTCCCTCCCATCTCTGGTCTTTAGT
6675	Table 1	NA .	583G8	1	TGGAAGCAAGCTTTCGGACAACGG TCCAACAAGGGTTACGGCAGAATTTA
6676	Table 3A	NA .	584A1	1	TGCGAAAGTCTTCTTTGGGCTAAA TTGTTCTGCTCAGGCCAAGGATTGTT
8677	Table 1	NA .	584D3	1	GTGTGCTCTGTATTTGCTGCTTTG GGCCCGGCATGTCTTCGTTTTGTCAG
					TCCTCATCCAATCCATCTTCATAT
6678	Table 3A	NA	DNA sequence from clone RP4-620E11 on chromosome 20q11.2-12 Contains t	1	GTGGGTTTTTAGACACCTGCAGCAAG AAGAAATACTGACTGACTAGGCAT
6679	Table 3A	NA	591H9 ·	1	TTTTAAAGAAAAATCTATTATCTTGGA GCATGGATGGGGGAATGCGAAGG
6680	Table 3A	Hs.6179	DNA sequence from clone RP3-434P1 on chromosome 22 Contains the KCNJ4 gene for inwardly recitlying potassium channel J4 (hippocampal inward recitler, HIR, HRK1, HIRK2, KIR2.3), the KDELR3 gene for KDEL (Lys-Asp-Cilu-Leul) endoplasmic	1	CAGAAGAAACCAGGCAAACTGCTCTG TGCTTTCAAACCAAAGTGTTCCCC
			reticulum protein retention receptor 3, the DDX17 gene for DEAD/H (Asp-Glu- Ala-Asp/His) box polypeptide 17 (72kD), ESTs, STSs, GSSs and six putative CpG islands /cds=(307,2259)		
6681	Table 1	Hs.44577	602388170F1 cDNA, 5' end /clone=IMAGE:4517129 /clone_end=5'	1	GTTACTTAAGATCAGTATGTGTGGTG CATATGTGATTTCGACCATTCAGT
6682	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	1	GAGAATTTCCGTCTGATCTATGACAC CAAGGGTCGCTTTGCTGTACCTCG
6683	Table 1	NA	119F12	1	CTGGGTTAATACTCACCAACTTTGAG AAGGTTGGTCTCTGCTCTTCTGTA
6684	Table 1	NA	119G10	1	GGAAAGACAGGTGAGTGTGCCACAA CTACCTAACACATCAGCAAATCTGG

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					Table 8		
6685	Table 1	NA			485A6	1	GTCACTTTAGCGAGCGGGAAAACAAT GGCGGAAAGGGAAAACCTGGAAAG
6686	Table 1	NA			485D5	1	CGATAAGCTGTGGTGTTGGGAGTGA GAGATGTTACTTTGCGAATGTTCAA
6687	Table 1	NA			489H9	1	AAAGGCTAGGTTTGCGAAAGCCCTTC TAAAACTATGCTTTGGTGGTTACT
6688	Table 2	NA			494B11	1	CTGACCCTGCCGGGCGGAAGATAAA ACAAAAACGAGAAGAACAAGCAAGA
6689	Table 1	NA			478E5	1	AAGATTGTAAAAATACATTTTAGGCTC AAGAGTTCCAGGGGTTTCAGAGC
6690	Table 1	NA			478G6	1	TGCAAGCTGGCACCTTCACGTTTATT TTTAAAGGGCTTCACATCAAAGAT
6691	Table 3A	NA			478H3	1	AAACAAAGAAGGAAAATGAAGAGGG GGAAAAGATGAACATCAGGCTGGGT
6692	Table 1	NA			478C7	1	TCCAAAGGATGTTCTGGTGTTTGCAGC ATGATTTCTGGTGTTAGTCTTTCT
6693	Table 1	NA			478G8	1	TTTGTGGGTGCGTGAGAGGGGATTTA TACTCCTTGAGCCATATTTTGTGA
6694	Table 1	NA			478H7	1	GGGTTCACAGCATGGGTGGAGGTAA GTAGTATTCTCATTGGTTGGTTAGT
6695	Table 3A	NA			479B4	1	GACAGTGAGAAGAATATGGAGTAGA GTCCTTTTGGTCTTTGAGGCGGTCA
6696	Table 1	NA			479D2	1	AACAGCTGAAGAACAAGAAGGTGAG CTCTGAATGCGTCAGGTGGTCATTC
6697	Table 1	NA			479G2	1	GGCTGACCAGTACAGGCTTGGGAAT TITATGGTTGGGTGGTTCTACCAA
6698	Table 1	NA			479G3	1	GGGGGAGCTATATTACTGATTAAAAC CACCATTTCTTCACCCAACTTATG
6699	Table 1	NA			479G5	1	AAGTCTTGTATTATGAGGTACTGGGG CTCTGGGGGATATTGAGATGAGA
8700	Table 1	NA			479G6	1	AGTCCTGCTGAATCATTGGTTTATAG AAGACTATCTGGAGGGCCTGATAG
6701	Table 1	NA			479H4	1	GGAGCTTCCAGTCTAATAGAAAAGAT GCACTTACGAATAGACTTTGGGTA
6702	Table 1	NA			479H5	1	TCTGTGCTCTGTGGACCCGTCACCCT GAGCTCCTCAGTTGCTGAACCATC
6703	Table 1	NA			479H6	1	TGCTGGCATGTGGATAGACTTTAGCA AATGGTAGTCATCTTCTAATTTCT
6704	Table 1	NA			479G12	1	AATGGGAATCTTAAGGCCTCTCTGGA AAGGGTGTGAGGGGGGTCGAGGGGG
6705	Table 1	NA			479H12	1	TGCATATTGTCACTGACTGGCTAGGG TCTCTAAATTTATGAAACCTTACA
6706	Table 1	· NA			482A5	1	GTCAGCAACTAAAAAGGGAGATATAT CTTAGAGAGACTGGAATAAGCAACTC
6707	Table 3A	NA			483G5	1	GGAAGGACTCAAACTGGCCATAAAG GCAATACGGCATGTTCATTACACCA
6706	Table 1	NA			486C4	1	TTTGTTGACTATGAAATAGTGGTCCT GGTTTTAACTCTTTTGGGGTTCCCT
6709	Table 1	NA			490F10	1	AATTATATTTTAGGCTGATGTGGGTG GTCTGTAATGCTCTCATTTACCAC
6710	Table 1	NA			493C2	1	CTGTGTTTCTGTATGGTATTGCATTTG TCCCGGCCTGTTGGGTTTGGTGG
6711	Table 1	NA			58G4	1	TTCATGCTCATTAGGACATTGAACAA ATGGCAGAGTAAGAAAGTTTGGCC
6712	Table 3A	Hs.169370			DNA sequence from PAC 66H14 on chromosome 6q21-22. Contains FYN (P59-FYN, SYN, SLK) gene coding for two isoforms. Contains ESTs and STSs /cds=(12,1706)	1	GGGAATGGACTCATATGCAAGATTGC TGACTTCGGATTGGCCCGATTGAT
6713	Table 1	NA			598H2	1	CAACACATGGGACGGGAAGGAAATC
6714	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10, mRNA sequence	1	CTTCCGTGTGATTTTGTTAAAAATA CAGCCACCTCCTCAGGTCAGACAAG CCCAGCACCCAAATACCACTATCTG
6715	Table 3A	NA	AA501725	2236692	mRNA sequence ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element;, mRNA	1	GGCTTCCCTATTACCTCCCAGCGAAA TTCGTAGTCTTTCTCTATGGAGTT
6716	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	1	TGCTGATGTGTTAGGTAGTTGTGGCA CACTCACCTGTCTTTCCTAAATGC
6717	Table 3A	NA	AA579400		nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915561 similar to contains Alu repetitive element;contains	1	TTCATGCTCAGCAAAACAACGTTTTA GGATGGTGAGAGAAAGAAAGTAA
6718	Table 3A	NA	AF249845	8099620	isolate Siddi 10 hypervariable region I, mitochondrial sequence	1	TATTAACCACTCACGGGAGCTCTCCA TGCATTTGGTATTTTCGTCTGGGG

Table 8									
6719	db mining	Hs.277051	Al630242	4681572	ad07c09.y1 cDNA /clone=ad07c09-	1	TTACCTGCTTTGCATGCTCTCCATCG		
6720	db mining	Hs.277052	Al630342	4681672	(random) ad08g11.y1 cDNA /clone≃ad08g11-	1	TCAAAGTCTTCTGGAAACTTAGGC CCCCACCCCAACACATACAAACGTTT		
6721	db mining	NA	AI732228	5053341	(random) nf19e05.x5 NCI_CGAP_Pr1 cDNA	1	CCCACCAATCCTTGAACTGCAAAA TTCAAGGTCCCAATACCCAACTAACT		
	as many				cione IMAGE:914240 similar to contains Alu repetitive element, mRNA s		CGAAGGAAGAAATGGAAATCTATT		
6722	Table 3A	Hs.197803	AW379049	6883708	mRNA for KIAA0160 gene, partial cds /cds=(0,2413)	1	TGCACAGAACTCTTACTTACATGTCT CATCGAAACTCCAGAACACCGTCG		
6723	Table 3A	Hs.232000	AW380881	6885540	UI-H-BI0p-abh-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035	1	TGCATGTATCCCGGTAATTCAAATCC AATTTCACAGCCACTGCTGAATAT		
					/clone_end=3'	1	TACAGGAAAATGAAACTAGACGGGTG		
6724	Table 3A	Hs.325568	AW384988	6889647	602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	1	GGGGACACTAGAATGAAAACCAGT		
6725	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030	1	AGTTTCTGCTTTCAGTGACTGAGGCT		
6726	Table 3A	NA	AW837717	7931691	cDNA, mRNA sequence CM2-LT0042-281299-062-e11 LT0042	1	TTGCTTTAACCTGGTGACTCCCAA TCCCACTTCAAGTTAAGCACCAAAGC		
	Table 3A	NA.	AW837808	7931782	cDNA, mRNA sequence CM1-LT0042-100300-140-f05 LT0042	1	AATCACTAATTCTGGAGCACAGGA CATGGATGGGGGCAGTGGTGTTTCT		
					cDNA, mRNA sequence	1	AGTGTGTGAGGAAGCAGAGCAGATG TCACCACAGATGGGAAGATCGTTTCC		
	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence		TGAAAACAGTCTATAAATCACAGA		
6729	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	1	CAGACGCTCCAGTGCTGCCGAGGTT AGTGTGTTTATTAGACCTGAAATGA		
6730	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	1	CCCTTTAGGCCTCTTGCCCGAACAGT GAACACTAATAGATATCCTAAGCT		
6731	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	1	ATGGGGATCATGTTTTATTTTTCTCTA TATAATGGGCCAGTGTGTTCCCA		
6732	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041	1	AGCTGTAGACCATAAGCCACCTTCAG		
6733	Table 3A	NA	BE086076	8476469	cDNA, mRNA sequence PM2-BT0672-130400-006-h09 BT0672	1	GTAGTGGTTTGGGAAATCAAGCAA TGTACTTATGCTTGTCTTCTCTACCTG		
6734	Table 3A	NA	BE091932	8482384	cDNA, mRNA sequence IL2-BT0733-130400-068-C11 BT0733	1	CCCCCAGTCTTGAAGTGGTGGAA GGAGGGTGTGGGAAGCAAGAGAA		
					cDNA, mRNA sequence		ACATTCTGTTAGGGGCAGAGAAGAA		
6735	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2),	1	GCATCTCCAGCTTTCATAGTTACCCA ACTTGTAAACCAGAAGATGTGCTG		
			DE10-10-		mRNA /cds=(0,1922)	1			
6736	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence		GGCCAGTGCCAGACGGTAGCTAGTT GGATGCTAAAGGTAGAATTTAGATA		
6737	Table 3A	Hs.301497	BE166334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced	1	GGCATTGTAGGTTGACACCAGCAAAG ACTCAGAGTGACTTGAGCATTGGA		
					product, partial cds /cds=(0,1544)				
6738	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	1	AGCCCATTTGGATATGGCCCATCTTT ACCTAATGGCTACTATAGTGAGGT		
	W. b		DE422004	0070040	_	1	AATCACAGCAGTAACTCCCAGTAGGA		
6739	Table 3A	NA	BE177661		RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence		AAGATTCTCAAAGGAATAGTTCTT		
6740	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	1	AATGGTCAGGCACAGGTAGAATCAAA GTCCTGTATGTATGTTCACACAGA		
6741	Table 3A	NA	BE247056	9098807	TCBAP1D6404 Pediatric pre-B cell acute lymphoblastic leukemla Baylor-	1	TACCTGAAGGTGTAGAGAGTGCCCG CATCCAGCAAGGCCAACAGCTCCAC		
8742	Table 3A	Hs.11050	BE763412	10193336	HGSC project=TCBA cDNA clone T mRNA; cDNA DKFZp434C0118 (from	1	CTGTGTTTTTCCCAAAGCAACAATTTC		
0742	Lapic ov	118,11000	BE703412	10100000	clone DKFZp434C0118); partial cds		AAACAAAGTGAGAGCCACTGACA		
6743	Table 3A	NA	BF330908	11301656	/cds=(0,1644) RC3-BT0333-310800-115-f11 BT0333	1	GACTCCGAGCTCAAGTCAGTCTGTAC		
6744	Table 3A	NA	BF357523	11316597	cDNA, mRNA sequence CM2-HT0945-150900-379-g06 HT0945	1	CCCCAACCCCTAACCCACTGCATC TGTAACTGACTTTATGTATCACTCAAG		
6745	Table 3A	NA	BF364413	11326438	cDNA, mRNA sequence RC6-NN1068-070600-011-B01	1	TCTTGCCTTTACTGAGTGCCTGA TCTCTCTAACCAAAACTGTAATCTTCA		
6746	Table 3A	NA		11335663	NN1068 cDNA, mRNA sequence	1	GGACCAGCAAACTCAGCCCAAGG AACTCTTGGTTAAATGGGTTAATAGA		
6747	Table 3A	NA.		12067339	cDNA, mRNA sequence QV1-HB0031-071200-562-h04 HB0031	1	GGATTGGAACACTTTGTTTGCTGT AGAAGCAAACCTGTGAAGCTACTATC		
					cDNA, mRNA sequence		GTTTATCATCAGTGTGAATGCACT		
	Table 3A	NA		12075765	MR2-BN0386-051000-014-b04 BN0386 cDNA, mRNA sequence	1	GGACTAACTTCCACCTCCTCTGCTAC TTCCAGCTGCTTCTAATCACACTT		
6749	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	1	AGTCTTCCACCCAGCATAGGTATCAC ACAACCAGCTCTGTTTTACTCCTG		
6750	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	1	TTAGCTGGTACATTGTTCAGAGTTTA CTGGGAGCCGGTAAGATAGTCACC		
6751	Table 3A	NA	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	1	AGCGTGATGCTTCCTCATGTCGGTGA TTTTCTGTTGAGACATCTTCAAGC		
6752	Table 3A	NA	BF805164	12134153	QV1-Cl0173-061100-456-f03 Cl0173	1	CAGGGTTAACAAAAGTATGGAATTCA		
					cDNA, mRNA sequence		ATTCTTTTTATATGCTGCAGCCATGTT CCT		
6753	Table 3A	N A	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	1	TGTAATTGATTTCCGCATAAACGGTC ATTACTGGCACCTATGGCAGCACC		

	WO 02/0:	5/414					PC1/US01/4/856
					Table 8		
6754	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08	1	GTGATCCACTTGGAGCTGCTACTGGT
6755	Table 3A	NA	BF845167	12201450	HN0025 cDNA, mRNA sequence RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	1	CCCATTGAGTCCTATAGTACTTCA TGCCATGAAATCTCTATTAATTCTCAG AAAGATCAAAGGAGGTCCCGTGT
6756	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	1	CCCACCTGGCAAATCCTCAAGTGTGA CCCTAGTCATCTTTCTCCTTTTGG
6757	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	1	GCTAAACAGAAAAGAACCTGAAGTAC AGTTCCCGTCTTCAAAGAAGATGC
6758	Table 3A	NA	BF877979	12268109	MR0-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	1	ATCCTCCTCCCCTGGGATGGCATAGA AGAGACTTTAAAACCAAATGAGCC
6759	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	1	GTCAGTAAGCTCTGCCTGCCAAGAAG ACACAGTGAGAGGTGTCCACAGTC
6760	Table 3A	NA	BF898285	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	1	GTTTCCACTTAGTTACTTCTTCCTACC TGCTGTGAAGCTCTGCACCCTGC
6761	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	1	AGAGTAATCCACATCCCAGGGACAGT CACAATGACCTACGGCTTTAGCTG
	Table 3A	NA	BF904425	12295884	CM1-MT0245-211200-662-d02 MT0245 cDNA, mRNA sequence	1	GCAGGGCTACACCAAGTCCATTGATA TTTGGTCTGTAGGCTGCATTCTGG
6763	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	1	TCTTCTCTAAAATGCCCTCCTCTCTT CCTTTTTCCAGACCTGGTTTAAA
6764	Table 3A	NA .	BF926187	12323197	CM2-NT0193-301100-562-c07 NT0193 cDNA, mRNA sequence	1	TCGCCATTTGGTAGTTCCACAGTGAC TGCTCTTCTATTTTACGAAGCCAC
6765	Table 3A	NA	BF928644	12326772	QV3-NT0216-061200-517-g03 NT0216 cDNA, mRNA sequence	1	GTAGATTACTATGAGACCAGCAGCCT CTGCTCCCAGCCAGCTGTGGTGTG
6766	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	1	TTTCCTTTTCGCTGACTTTCTCACTCA CTGTCTGTCTCTCATTTTCTCCA
6767	Table 3A	NA	F11941	706260	HSC33F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	1	TGGTAAGTTTCTGGCAGTGTGGAGAC AGGGGAATAATCTCAACAGTAGGT
8768	Table 3A	· NA	U46388	1236904	cell line Patu 8988t cDNA clone xs425, mRNA sequence	1	CCATGGTGGTGCTTGACTTTGCTTTG GGGCTTAATCCTAGTATCATTTGG
6789	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	1	TCAGTGGGTGTTGGTTGTCCATTAGT TGAGACTTAGTTGTTGCTCTGGGA
6770	Table 3A	· NA	W27856	1307658	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	1	GGCTGGACAGCAGATGATTCAAATCT CAATACTACATGCCCATTCTGTGG
6771	Table 3A	NA ·			36G5	-1	CAGGATGGAACAAGACTCCAGCCCC TGCCTGTCTCATGTATCTGCAAGGG
8772	Table 3A	NA			36F11	-1	CTTCAGTGCGTACACGAGCTCAACGT TAGTGCCAGGAAAGACAACTACTC
6773	Table 1	NA			37G7	-1	ACTCGTATGCCAACTCTTCTGTCTTC ACTACTAGAGTGTAGATTGGACTC
6774	Table 1	NA			37G8	-1	TGGACTGGAACTTGACTCGAAGTTAT GTGGCTTAATGAGTAAGTTCAGCC
6775	Table 3A	Hs.197345			thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA /cds=(17,1846)	-1	ACTGGTTCATTTGTTTCCCGATAGAG CTTTATTGGAGGAGGCTTGAGAGC
8776	Table 1	NA .			40E4	-1	ACCATCTCCTTTAATCCTCACAGTGA TCCTGGAGCAATGTGTGCATTCCT
8777	Table 3A	NA ·			41E9	-1	CATCACCTGCTCACCTAGGAACCAGG AGTACTGGGAACTGTTCCGTTACT
8778	Table 3A	Hs.169478			Homo sapiens, glyceraldehyde-3- phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313)	-1	TCATTGCTGATGATCTTGAGGCTGTT GTCGAACTTCTCATGGTTCACACC
6779	Table 3A	NA			47E5	-1	TGGCACCACGCTGATTATTTTCCTTTT CAAATCCCAGCCTATACACCTCC
6780	Table 2	NA			47D11	-1	GCTGTCTGTCTTCCCAATATCCATGA CCTTGACTGATGCAGGTGTCTAGG
6781	Table 1	NA			50A11	-1	AGGCCTTTTTATTTGTCTGTTTAGATA CACTGCTTCCTATATCTGCTGGA
6782	Table 3A	Hs.132906	•		DNA sequence from clone RP11- 404Fil on chromosome 1q23-1-24.1. Contains the 5' end of the SLAM gene for signaling hymphocytic activation molecule, a SET (SET translocation (myeloid leukemia-associated) protein pseudogene, the CD48 gene for CD48 antigen (B-cell membrane protein), the gene for a novel LY9 (ymphocyte antigen 6) Rei protein and the 5' end of	-1	CCCGTSCCCCACCACTCTCACTGC TGACTCCAAGTCTCGTACACTAGAT
					the LY9 gene. Contains ESTs, STSs and GSSs /cds=(41,1048)		
	Table 1	NA			52B9	-1	AGCGATGAACTGTTGCAAAAGAATTT TCCAGAGCATTTTCCATTAAACCA
	Table 1	NA			53B1	-1	CCATATTCTTGTTCCCCAGCCAGGTG CTGCACCTCCCCACTCTTTTAGTG
6785	Table 1	NA			63E3	-1	AAATGCTTAAAGGAACAATATATGTC CCTTTCGAGGCACGTGATTCGTTT

			Table 8		
6786	Table 1	NA	53E10	-1	TCTGGAGCCACACCCTTACCATCACC
6787	Table 2	NA	53G7	-1	TTCCAAAGAAGAAATTGAACCCTT AATCACACAAGGTCGAAAGTAGACAG
6788	Table 1	NA	54F4	-1	TCCTCTTGGACTTGGAATTGTCCA ACTTTCCTCCGGGAAGTTTGTATCTT
					AGCGTGGACAACAGGTTAACACAA
6789	Table 1	NA	54G9	-1	TCAGGATGCTCTCACTTTAAGAACCG GGCAAATAATAGAACACTGTGACA
6790	Table 1	NA	59G1	-1	ACTTCACTCAGAGTAAATGAAAAGAC TGGGTGCCTCATCAATATCATTGT
6791	Table 1	Hs.48320	mRNA for ring-IBR-ring domain	-1	TGACTGAAGGCAAGCTCACAGATGAA
			containing protein Dorfin, complete cds /cds=(317,2833)		GCAGAGGACTGAAGATCTCGATCT
6792	Table 1	NA	60G8	-1	GCTGAGAAGGATGTGGTATAAATGTA TTAAGCAGCTTAGGGTCTCTGGCC
6793	Table 2	NA	62C9	-1	AAGTCCCCGTCTAGTGGGAAAGAAA GAAGTTGAACAAGTAATTCCAAGGG
6794	Table 3A	NA .	62F11	-1	CGCCCGGCAAGTACTGGGGTTTCTTA
6795	Table 1	NA	63E1	-1	TAGCTTCTCTCTGCATCTACAAAG CTGTTTCTCTATTTTAACTTACATTGG
6796	Table 2	NA .	65B1	-1	TTATTCTGTAAAGTCAGATGTGGCAG GCACTGTCCTTCCCAGTTCTACATTT
				-1	GAGTCTGAGTTGACTCGCAAGACT
6797	Table 2	NA	65D10		AACAGATTGTGCTTCTGTTCTGAATC TTCTAAAGCCATCTGCACAGTGCT
6798	Table 2	NA	65D11	-1	AACAGATTGTGCTTCTGTTCTGAATC TTCCAAAGCCATCTGCACAGTGCT
6799	Table 2	NA	65D12	-1	ATCTGCACAGTGTTAGCATGGTGACT CCAGTGTCCTCCAAGACTCCATAG
6800	Table 1	NA	68C9	-1	TTTAGCATCCACTAGTTACTGTCTGG
6801	Table 1	NA	69F8	-1	CACTGGCCACGAAGGGTGACAGGG GAATCCCGGTCATCTCTACCCAAGTC
8802	Table 1	NA	69H11	-1	CCGGTCTCTCTACCCTATTCTCTC TGGTAACTTCAAAGTCCCTAACACAT
8803	Table 3A	NA .	7086	-1	TCGATATTTCTCCTAGCTTCCACT ACTCCCACCAAACCCCACTTTGTAAT
				•	CACTGGTAGTAAAGAGAGATGCAG
6804	Table 3A	Hs.17109	integral membrane protein 2A (ITM2A), mRNA /cds=(139,930)	-1	AAGAGTAAGAGGCAACAGATAGAGT GTCCTTGGTAATAAGAAGTCAGAGA
8805	Table 2	NA ·	72D4	-1	GAAATTGGAAGGTGATACTTGGGGAC CACAACACGCACATCTGGGAACTG
8808	Table 3A	Hs.234279	microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA /cds=(64,870)	-1	TCATCTGTGGCATACAGAATGTCTAC AATCTTCTGCAATACAGGGTCGTT
6807	Table 2	NA -	72D8	-1	GGCAAGGGAACAAACTTGAGTAAATC
6808	Table 1	NA	73C4	-1	TAGCTCTTGAAGGGCTCGGGACCC ACTCATTTGTCTCCTCATTCTCAAAAG
6809	Table 1	NA	73H4	-1	TCTTCTGTGGTTTGGCTTCAGTG TCGATGGGCCATTATCCACTCTGCTA
6810	Table 2	NA	73A7	-1	TCTTCTGAAGAGTAATTTTCACCT AAGGACGGAACTCACACATCTTCTTT
8811	Table 3A	Hs.174228	small inducible cytokine subfamily C,	-1	AGACAGAAATGTAGTCTCACTGCA TATAATCCCAGTCCATGAGGGTGTAA
			member 2 (SCYC2), mRNA /cds=(0,344)	Ċ	AGTGAAATGAGCTGGCTGGCA
6812	Table 3A	Hs.3945	CGI-107 protein (LOC51012), mRNA /cds=(84,719)	-1	GCTCTGTTCTGGGGTTGGTCCAAAGT CAGGTGGAGTTCCAATGTATGAAA
6813	Table 1	NA	75A2	-1	TCCCTGAGATCTAGGAGGGCAGCAT AGTATCATTTTTGTATTCCGGTGCT
6814	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA	-1	AGCTGCTACAAAGAAGACATGTTTTA GACAAATACTCATGTGTATGGGCA
6815	Table 2	NA	/cds=(104,1222) 75B12	-1	AGGGATCTGAATACTTCGGGTGCAAA
6816	Table 2	Hs.205442	601439689F1 cDNA, 5' end	-1	AATTITCCTGCAGTTTAGATTTGC TATGGTTTCCAATATCGACATGGCAT
			/clone=IMAGE:3924407 /clone_end=5'		CATTGGTTACATTAGCACTGGGCC
6817	Table 3A	NA	101G7	-1	GGCCTGGGCATAGACTGTGGTGAGG
6818	Table 3A	Hs.179565	minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3),	-1	TCACTAGATTATCTTGTTCTTCCCC GAGTCCTGATCTCAGCTTCATCACCA ACATTCCTCGCCTTCAGTTGAATT
6819	Table 1	Hs.119640	mRNA /cds=(44,2470) hBKLF for basic kruppel like factor	-1	GGAGGTCTTTGCCACCAATGGGAGA
6820	Table 3A	Hs.215595	(LOC51274), mRNA /cds=(55,1092)	-1	TGAGCCCAAACTTTCGATATAGGTG ACCAGAGGTAAACTTGAGTGTAATTG
			guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA /cds=(280,1302)		TCAGACAGACACACTTTTCCACCA
6821	Table 1	NA	105A10	-1	TGCATTTTACATTAGCTTCCAATATTT ATGGCAGTAACCAACAGTATTATCGT
6822	Table 1	NA .	107G11	-1	TTTCCAATGCTCCTTGCTCCATTTTAA ACTTGCTGTCCTTTATAAGAGAA

			Table 8		
6823	Table 1	NA	107H8	-1	TGTTTTCACGATAGAAATAAGGAAGG TCTAGAGCTTCTATTCTTTGGCCA
6824	Table 3A	Hs.64239	DNA sequence from clone RP5- 1174M9 on chromosome 1p34.1-35.3. Contains the gene for a novel protein with IBR domain, a (pseudo?) gene for a novel protein similar to MT1E (metallothionein 1E (functional)), ESTs, STSs, GSSs and two putative CpG islands /cds=(0,2195)	-1	TTTCATACAAAGCCAACAGAATTCAC AGCCACACACTGCACAGGTCATGT
6825	Table 1	NA	109H9	-1	AGGAAGCTGTGAGGGTGGGTTCATT AGTTGCAGGGATGGTAGTTATGTCA
6826	Table 3A	Hs.80261	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related) (HEF1), mRNA /cds=(163,2667)	-1	GAGACAAGCTGGAAGGCCGGACCTC AGACCGGAGGGGGTTTATGTCATTC
6827	Table 3A	Hs.1422	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), mRNA /cds=(147,1736)	-1	ATAACTAGACAAGGTCTGAGCACTTT GGGTGGGGATGGAGTGAGAAAGGC
6828	Table 3A	Hs.333114	AV713318 cDNA, 5' end /clone=DCAAAC09 /clone_end=5'	-1	ATTAAGTTGGGTAACGCCAGGGTTTT CCCAGTCACGACGTTGTAAAACGA
6829	Table 1	NA	129A12	-1	GCGTTCTAGCTGGGCCAACAGAGCA GGATTTCGTTTCAGAAAACAAAAC
6830	Table 1	NA	129F10	-1	ATCATGTCTCATTAACAGAGTGAAGA TGGAGCAACGTCATCCAGCTTCTG
6831	Table 3A	NA	137D4	-1	TGGTCGCGCCCGAGGTACGGTTTTC ATGGTAGGGCTGAATGGAAGATGTG
6832	Table 1	NA	142F9	-1	CAGAAAGATAGGAGTGTGCAATGGC AAGGAAACTCAATTTAAAGCAAATT
6833	Table 3A	Hs.250855	Prothymosin, alpha (gene sequence 28)	-1	TTGCAAATTCTCATGGTTTGGGTTGG GTGGTGGAGAGCGCGTGTCATCTG
6634	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222)	-1	TTATTCAGCGTCACGATCAGACTGTT ACATTTAGCAATCAACAGCATGGG
6835	Table 1	NA	149G2	-1	TGTGTGTATGTGTGTAACCAGGTCTG ACTATAGCTTGGTCTGTCTGTGTC
6836	Table 1	NA	149A11	-1	AGCATTTGGGGTTTTTAGCTTTGGTGT CCTAAATTTCAGTGATCTTTGCCA
6837	Table 3A	NA ,	151F11	-1	CATAAACCAGCAGCTCAGCGTTTCTA TAGCAAGCGGTCTCGAGCACAAGC
6838	Table 1	NA	162E8	-1	TAGTGATAGGCGTGGTGGCGGCGAA GGTCAGTAATGGGGCTTTTAACCAG
8839	Table 3A	Hs.334330	calmodulin 3 (phosphorylase kinase, delta) (CALM3), mRNA /cds=(123,581)	-1	TACTGTAGAAAGAAGAAGAGCACACA TGAGACAGAAGAAGGAGGTGGATGC
6840	Table 1	NA	170F7	-1	CGAGGCGGCCCGGCAGGGTACCAAT TTGGATGAATTCTTGATAGATTTAA
6841	Table 2	NA	170F9	-1	TTGGGTTCAGAATAGCTTCATCTACT GCCGAGCAAAGTCAATACAGCACT
8842	Table 3A	NA	177A3	-1	GGTAACAGCCATCCCACCACCAATAA TCATCTCATTGTCTTTGTCCAGCA
6843	Table 1	NA	331A3	-1	GTATGAATAGATTGCCCCATTCCCTG CCAGCCTGGTAGTGACTTTTCCAC
6844	Table 1	NA	331A5	-1	TATAATTTCTACCAAACTAAGTTTTAT TTTGTGCCCGCTCCCTGTCCCTT
6845	Table 3A	NA	146C3	-1	CTGTAAAATTCTTTTCGGGTCCATCC TGGCTCTCATCTCCAGTGCTTTGA
6846	Table 1	NA	146D8	-1	AGGGTTAACAAAAGTATGGAATTCAA TTCTTTTTATATGCTGCAGCCATGTTC CTG
6847	Table 3A	Hs.153	ribosomal protein L7 (RPL7), mRNA /cds=(10,756)	-1	CCCAATCTGAAGTCAGTAAATGAACT AATCTACAAGCGTGGTTATGGCAA
6848	Table 1	NA	158G6	-1	CCGAGGTACTCTCTTAGAGAAAGGTG ATTGGATGCTCCGGTTGCCTGTAA
6849	Table 1	NA	158H6	-1	GCGGGTTGGAAAATAGTCGAGAATTG ACAGTCCCTCTCGAAGATGCTTTT
6850	Table 3A	Hs.119598	ribosomal protein L3 (RPL3), mRNA /cds=(6,1217)	-1	TTGAGACCCCACCAACTGCAAAATCT GTTCCTGGCATTAAGCTCCTTCTT
8851	Table 1	NA	158G11	-1	AATGAAAAACTCCAGCTCTCAGCTCA CAAATCTGTAATTTAGGTGTCTCT
8852	Table 3A	Hs.326249	ribosomal protein L22 (RPL22), mRNA /cds=(51,437)	-1	TCGTCCTGGTTAATCTGGAAGTAACG TAATTCGTAACTCTCTTTGCTGTT
6853	Table 3A	Hs.297753	vimentin (VIM), mRNA /cds=(122,1522)	-1	TCGGTTGTTAAGAACTAGAGCTTATT CCTATTCCAAATCTATCTTGCGCT
6854	Table 3A	NA	155H10	-1	AGATAAGAACTTCATCCTAAAGCATC CGGGCCTTGGCATCTTGTCCATGC
6855	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	-1	ACTGATTTCATCAAGTTCGACACTGG TAACCTGTGTATGGTGACTGGAGG
6856	Table 1	NA	159F6	-1	AATCATTGGCTACCTCCCCTTTT ACAGTCACAAGTCCAGATGTTTGG

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			Table 8		
6857	Table 3A	NA	166F3	-1	AATAAATCCCATACCTCCCATTGAAC TACCACCCACCCCGACCACCATAA
6858	Table 1	NA	166F6	-1	CAAGACATTTCCAGCCAACTTCAGAA TGTAGATCTTTGAGCCAGACAGCT
6859	Table 1	Hs.8121	Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427)	-1	GAGGTACTGGCCTGTGAAGCCCTGA AGGCACTGGCACTGGTAGGAACCAG
6860	Table 2	Hs,25130	cDNA FLJ14923 fis, clone PLACE1008244, weakly similar to VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 /cds=UNKNOWN	-1	ATCTTCTGTCAAAGTCAGTCGCTGCT CCAAGATTGAAACAGTCTGTGTCA
6861	Table 1	NA	168A9	-1	TGGATGGATTTCCAAGTGGCCTCATA TTTATCATGGTGCTTTAAATAGCA
6862	Table 1	NA	171F11	-1	TTCAGCTTAGGGAAAGAGAGATACAT TTTAGATTATAGAGCATCGCCTGC
6863	Table 3A	NA	171G11	-1	ATCTTCCTATGTGCGCCAGATAATGA TCAAGTTCACAGGTGGTCTTACTT
6864	Table 1	NA	175D1	-1	AGTITCTTAAGTCAAATGACACATTAG CCCACGCAATTCCCAGCCCCAGC
6865	Table 1	NA	182H1	-1	CCCTCTTCTGACATGAATTAGGCATA ATTTAGCAATCGGTTCTTCCCAAA
6866	Table 3A Table 3A	NA NA	184B5 184D2	-1	ATACAGTGAACTGGCCACTGGCTGTT TGCTATATAAATGGTATACTGCTT AGGTTACTTAAAAGCATCATTGGCGT
6868	Table 1	NA NA	184H1	-1	GGTCCTCTCACTACCAAAGGGCAG CTGGGGTCAGCAAAGAGGGGTAGCA
					AGTGTGCCTTAGAGATGAAGAAATG
6869	Table 1	NA	46D1	-1	TTTAGAGTACTTAGAGGAGGACCAGG AAACACTGAGACAGACACGCAGGC.
6870	Table 1	NA	98C1	-1	TGTTTGAAAACTACCTTCATGGGAGC AATGACAAGCACATGTCTAGGATT
6871	Table 1	NA	98C3	-1	TTTGTGCCAAGGTTTGGGATTTTGTC TTCTAGAGCTTCTTCTCTATTGGT
6872	Table 2	Hs.205442	601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5'	-1	TTTTTGACGCTCTCTCACTGGTCTTG GCATTTGATGTTTCTGTTGAAGCC
6873	Table 1	NA	98H4	-1	CCTATAATGGGGGAAAGATGCTGGTT AGATGTTTATTTTAGTGGGCTTGC
6874	Table 1	Hs.169363	GLE1 (yeast homolog)-like, RNA export mediator (GLE1L), mRNA /cds=(87,2066)	-1	CCACAAACACACCCTGCCACAAGACA TTTAGCACAGAGGAACAGATCCAT
	Table 3A	NA	113F12	-1	GACACCACAACTCACCTCCTCTATTA TTAGAGATCCCGAGACATTACGGC
6876	Table 1	Hs.30212	thyroid receptor interacting protein 15 (TRIP15), mRNA /cds=(15,1346)	-1	TGTTACAATTTCAGCAGTTGAATTCA GTGAACACTGGTTGAGGAGTGCCT
6877	Table 3A	NA .	173A10 hypothetical protein FLJ23544	-1	CCTTCCGTATTCTCCCAAGTATTCAC AAGCCCTCCCTTAAAACCCTCTCT ACAGCCATCTGGGATGAGCCGCTTTT
6879	Table 3A Table 3A	Hs.334853 Hs.20252	(FLJ23544), mRNA /cds=(125,517) DNA sequence from clone RP4-	-1	CAGCCATCTGGGATGAGCCGCTTTT CAGCCACCATGTCTTCAAATTCAT TAACTGAATACAGTCTCATCTTGCCG
00/9	Table 3A	119,20202	648B12 on chromosome 1q42-11-42.3. Contains an FTH1 (femtiln, heavy polypeptide 1) (FTHL6) pseudogene, the gene for a novel Ras family protein, ESTs, STSs, GSSs and a putative CpG island I/ods=(0,776)	-1	CGCCTGGCTTACCTATCTGTGGAA
6880	Table 1	NA ·	174D1	-1	AGGTACTACACAAGGTGTCAGATGG GGTTGCCACAATGACTAGGACAAGA
6881	Table 1	NA	45B9	-1	CCAAGAAGACAGAAGGAAGTGTCGA ACACCATGACAAGAGCTTGCCAGAA
6882	Table 1	NA	45H8	-1	GAGAGCTTTCTCCCCGCCTTCAGTTT CTGATGGATCTAGCCATGTTGAAA
6883	Table 1	NA	111H6	-1	TAAAACTTTCTGCCAGGGTTCCAGAG AAAGAGTAATTTCCTTTGAGTACC
6884	Table 1	NA .	111E12	-1	CGCTCGCCGGGCCAGGTACCAAAAC TTTCATAATAAAAGGTAGGAAGGAT
6885	Table 1	NA	111H11	-1	TGACTTCATTGAAGGCTCCATCACCC AAAGTAGATGTTAAAAACCTTAAT
6886	Table 1	NA	112H3	-1	TTTATGTGGAAGGCTTCCCTATTACC TCCCAGCGAAATTCGTAGTCTTTC
6887	Table 1	NA	112E9	-1	TAAAATGTTGCCAGTGGAGGACCGAA TCAAGGTTATTGCTGACCTCATTT
6888	Table 1	NA NA	114G3	-1	AGATATGTTCTGAGCCCCGCCCACAC ACTGCCTGGTTACAGGGAGAGAAG
6889	Table 1 Table 1	NA NA	117H6 165E7	-1	GAGGTTCCTTCATCCCAGAAGAAGCA ACAGGATTTCCAGATCAGGGCAAC CTGGTCTGTGTCGTTGGCTTTATGAC
5890	I ADIC I	INO.	100m	-1	AGGAAGTGCCTGTGGCTTATCTTA

			Table 8		
6891	Table 1	NA	165E11	-1	CCCAACGCTTGTGTGCGTATGTATGT
6892	Table 1	NA.	165F7	-1	GTGTATTTAACATCCTGTTCCCAT GCATAAAGGCAGCCATTTCCATTCTC
6893	Table 1	NA	176A6	-1	TACATTCTCTAGTGATAGCAGAGG CGTTACGCAATGGAGAAGTCCCCTTG
6894	Table 1	NA	176G2	-1	AGGCCAAATCACCGCACAGTTGAATT
6895	Table 1	NA	176E10	-1	GCTGATTCTAATTGGTAACAATAA TTGTAGTGTAATTGTGTGATACGCAA
6896	Table 3A	NA	176F11	-1	ACCTTTAGTTAACCCAAGTGATGA CCTTGTTGCCGTGGGTATATGCATGA
6897	Table 1	Hs.232400	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230)	-1	TCTTACCTTTTGTTTGACTATGAA AAATGATATGTTAAGCACCCAAATCTT CACATGGAGGGGAAGGGGGTGGG
6898	Table 1	NA	71F2	-1	GGCCAAAGCTGTTTATTATGAGATCT TTGAGTGGAATCAGCATGTCTCCC
6899	Table 1	Hs.172028	a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715)	-1	TTAACAGCATTGAAGGTGAAACAGCA CAATGTCCCATTCCAAATTTATTT
6900	Table 1	Hs.180610	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein- associated) (SFPQ), mRNA /cds=(85,2208)	-1	AGGTACGAAAATACATTCTGGCATCA CACCCCTGAACCCAAGACTGTTCT
6901	Table 1	NA	124G4	-1	GAACTACCTACTGGCAGTTGGGTTCA GGGAGATGGGATTGACTTCGCCTT
6902	Table 1	NA	124C8	-1	AGAGCTAATATACAGAGTACCTGACA CACTACCTCACCAACAGTTTAACT
6903	Table 1	NA	124F9	-1	GCCCAGGCAACAAGAATACTTTTATC TTTGATCCGTTCTGTTTATCCAGT
6904	Table 3A	NA	127A12	-1	CTGAGGGTAGACTGTGGGCAAAGAG GACAACTCTCCCTCCCTAAGGGAC
6905	Table 1	Hs.50180	601652275F1 cDNA, 5' end /clone=IMAGE:3935610 /clone_end=5'	-1	TGCCCAGACCTATTTCCTTAGGACAG TATTCTAAAGTTCAGTAGTCCAGT
6906	Table 1	NA	161E8	-1	GCCCTGTCCCTTGAGAGGCTCACAG CGATGGAGGCCACTTTTGTTGTTTG
6907	Table 1	NA	186E8	-1	ACCAAAAAGGGCTACATTACCACCAC TGTATCATAAAAGCCAGCCACCTT
6906	Table 2	NA	191F6	-1	AGCTGACGATTTTCTATCCCGGCCTA TAGTGCATGTATGGCAATTGAGCA
6909	Table 3A	NA	193G3	-1	CCCCAAAACAAACAAATAAACCACA CCAGATATCAGTCACATCCTTGAA
6910	Table 1	NA	194C2	-1	AGTCTGTTATTGCCTGATTTTGTCCC CACCTTGTTCAAATTTCCAAAGCT
	db mining	NA	458C6	-1	CTCACAGCCGAAGCTCTGATCCTTTG TTCTCAGGAAACACTCAGGAAGTG
6912	Table 1	NA	458E4	-1	AGAGAAAATGAGAGACAGACAGTGA GTGGGAAAGTCAGCGAAAAGGAAAA
6913	Table 1	NA	458G10	-1	TCCTTGAGTTTATACACCGTGCTATG AGTGATGACAGCCAATTCCCATGC
6914	Table 1	NA	459B3	-1	TCGCTTCAGGGGTCAGCCAAAAGATA GACAGCCAGGTAACTTGAGTGGAC
6915	Table 1	NA	459D2 .	-1	GGACAGTACCAAACACTCCCCTCCTC CCCTCTGCCTCTTTGCTTACTTAG
6916		NA	459E6	-1	GACCAAATACTGAACTTCCACCCTGC ATAATAATCATGAACACCGCACCA
6917	Table 3A	Hs.20830	DMA sequence from cosmid ICK0721Q on chromosome. Contains a 80% Robosomal Problem LSSA LIBE Profiles Robosomal Problem LSSA LIBE profiles Robosomal Problem LSSA LIBE profiles Robosomal Problem L12 LIKE profiles in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for a kinesin related protein, the PHF1 of the PHF2 gene coding for face different and LBM profiles Robosomal Profiles Robosomal	-1	AGGTGAGCAGTGCCTCAGATACCTG

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			Table 8		
	Table 1	NA	460B9 461A4	-1	CCAACCAAACCATCAAACAGCAGGGA GCTAGTGAAGAGGTCTATTGTTCC
6920	Table 3A	NA			ACATTCGCCTAAAACCGTGCATCGTAA ACATTTACCTCAAAGTCATCCTCT
6921	Table 1	NA	461 G 6	-1	TTTTCACTCCTCTCAGAGTCTACTCC ACCTCTCCTCACTCCCCAGGACAC
6922	Table 1	NA	461D9	-1	AGATCTGTGTTCGTCTCTAGGTAATA GGAAACACAATCCAGACATGATCT
	Table 3A	Hs.80768	chloride channel 7 (CLCN7), mRNA /cds=(38,2455)	-1	TTCATGAACTCGGAGAGGTCCATGGT GCACTCCCGCTCGTCCTGGGACAC
6924	Table 1	NA	461H7	-1	CTGGCAATATTAACTTGGGTTCTGTT TCATCTCTGGCTATAAGCCATACA
6925	Table 1	Hs.333513	small inducible cytokine subfamily E, member 1 (endothelial monocyte- activating) (SCYE1), mRNA /cds=(49,987)	-1	TGCCATTCTTTTGTTGAACCTGTAAA GGTAAGGCCCAGATTCTGAAACCT
6926	Table 1	NA	463A5	-1	TAAAGCACTTATGAGAATGCTGCATT TGTACATGAGCTACGCCTCATCTT
6927	Table 1	NA	463B2	-1	GCACCCACCTCCTCAGTTCAGACAAG CCCAGCACCCAAATACCACTATCT
6928	Table 1	NA	463C5	-1	AGCGCATGAGTGACTCCCATCTATAT ATGTCAGTCGTCTCTGGTGCAAGG
6929	Table 3A	Hs.40919	hypothetical protein FLJ14511 (FLJ14511), mRNA /cds=(22,1272)	-1	GAAACAGTGGCCCGGGTCGTAGTGC GCTGTCCAGATCTTCACGCTACACC
6930	Table 1	NA	463H5	-1	AGTGCATTCACACTGATGATAAACGA TAGTAGCTTCACAGGTTTGCTTCT
6931	Table 1	NA	463A7	-1	GCTTCAAAATTCCTTACCCCCAACCT CTGGCACCCCAAATTGTATCACTA
6932	Table 1	NA	463B10	-1	GAGGAAGGCTGGCTCTTACTCCCC ACAAGAGGTGTTCCTTAGGCCACAC
6933	Table 1	NA	463C7	-1	CCAATCTAATTTAAACCCTCATAACAG GACATAAGCTTGCGCCCGCATCT
6934	Table 1	NA	463F10	-1	TGCTCAATGTTTTGCACTGATTTTATT CAATGTTTTGAAGGGCGTTATGA
6935	Table 1	NA	464C2	-1	TGCTAACAACAGCTTCTCGGTATGTT AATATTCTGCTAACTCCTTTCTCA
6936	Table 1	NA	464C5	-1	GGAGGAATGGCTGTGCCCGTCCCCT CCACTTAAGCGACCTGAGTCTCCAG
6937	Table 1	NA	464C10	-1	ACACACACTTAAGAGTACAGATGAGA GCCAAAAATAAGTGGCAGGTCTTT
8938	Table 1	NA	464D8	-1	TTTTGTGACTGTGCATGCTTGAAAAG AATAAGTTTTCTGCAGCTGTGTCT
6939	Table 1	Hs.221895	7k30d01.x1 cDNA, 3' end /clone=IMAGE:3476785 /clone_end=3'	-1	CTTGTCTGTGGCGTGGCACACAGTA GGTGCTCGGTTTGTGTTGTTGAATG
6940	Table 1	NA	464E7	-1	GAATTCTGAATACATGTTGGACTGTG TTTCTTTGACCTGTGTTTCCTAGG
6941	Table 1	NA	464H12	-1	TGAGTCCTTGGCCTCAGCTTCTAATC TCAAACCTAAAATAGATTGCGTTT
6942	Table 2	NA	465B3	-1	TCTTCTCGTCTTTGCTATTAAATTTCT TCACGGACCATGCATCTGGAGGA
6943	Table 1	NA	465G2	-1	CCAGAGACTCCTAAGCAGAATCAAGG ATGTGTGGCATAAGCATGAGAGCC
6944	Table 1	NA	465H5	-1	CCCATAAAGAGGAATAAGCTACTGTC CTCAGCTCTTGTTAGCTCAGGCTT
6945	Table 1	NA .	465A12	-1	AGAGTTTGTAACACAATCCAGTCCAC ATGCTTATCCAATCCCATCATCCA
6946	Table 1	NA	465F7	-1	AGCTCAAAATATGGCAAAGTGATGAT TTCGTGTTAATCCTAGAAACAGCA
6947	Table 1	NA	465G8	-1	TGGGTCTGCTTTCACATGAAAGTGCT ACGAATTCTCTTTTGTGCTGAGCC
6948	Table 1	NA	465H10	-1	GGATGAGCCCACTCACAGCACCAGA TTTGTACTGAAAGTACCTTAATATC
6949	Table 3A	Hs.13630 9	DNA sequence from clone RP4- 612B15 on chromosome 1p22.2-31.1. Contains the (possibly pseudo) gene for a novel protein similar to 605 ribosomal protein L17 (RPL17), the gene for CGI- 81, endophilin B1 and KIAA0491, ESTs, STSs, GSSs and two CpG islands /cds=(1011,14/66)	-1	AACCCAAATCCAAATGCCAGGATAGA AGAATTTGTTTATGAGAAACTGGA
6950	Table 1	NA	515C12	-1	CGCTTTTTGATCTGATTACTATTTCAC ACAGGTTACAGCTATGACCATGA
6951	Table 1	NA	515H10	-1	CTGCCGCTAATTCACTAGTAATTTCG ATCGTCCGCCCTCCAGGTACATAT
6952	Table 1	NA	55G3	-1	AGGCGTGCTATTAATTATCCCATACC CTCCTTACAGAAATTACACTCGCA
6953	Table 1	NA	55F9	-1	GGGAGAAGTTCTTTAAACTAAGGGTA CAAAATGAATTGAAT
6954	Table 3A	NA	99E7	-1	ATTAGCGTGTTCGCGCCCGAGGTAC ACCAAAACCTTCAGAAAGCAAAGTT

			Table 8		
2055	Table 4	N- 04000E	103C4	-1	, AAGATATGAAATATGCCTACCCGCAG
	Table 1 Table 1	Hs.319825 Hs.17481	mRNA; cDNA DKFZp434G2415 (from	-1	AGCTTGGCACAAAGTGGAGTCAAT GTACAGAGATCGGATCACACAAGCC
			clone DKFZp434G2415) /cds=UNKNOWN		CGGAGACAGTGCAGCTTCTCCACTG
6957	Table 1	NA	116C9	-1	AATGCACTTGTGATAAACTGACAGCA GGGTTAGACATTACTTTCAAAGCT
6958	Table 1	NA	128F5	-1	CCACTGCTCAGGAAACTGCCTGTTCG GTGCTCCTCCAATTCAATT
6959	Table 1	NA	135F10	-1	AGTGCTGGTATAACTGCAGAAAGAGA TAGAGAAGAGAGATCAGTGAGAGC
6960	Table 1	NA	189F3	-1	AAGTCAGGACCTTTGCACTTGCCCCG CCTCTGCCTTCACAGCTCTTCTCA
6961	Table 1	NA	189A8	-1	TAATCAGGGAAGAGCTTGAGATCATT AGCAACTGAACTG
6962	Table 1	NA	195H12	-1	CTGGGTCACGTCGCCCACCAATGGT ATCTGTGTGGTTAGGCATTAGGCTG
6963	Table 1	Hs.292457	Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635)	-1	GGTGGTAGGTGAGTGGGTATTGCGG GCTAGTATCCGAGCAAAAGATGGTG
6964	Table 3A	NA	466C4	-1	CAGCCCTGCTATCTCTGGTTGTTCAT GTACTTCTGTAAGGTGGAGACCCT
6965	Table 1	NA	466D1	-1	GAAGGTGAGAAACCCGAGAGACACC AACTATGATTTTTACTTTTCCTGGT
6966	Table 1	, NA	466G2	-1	ACCACCCCTCCCTTCCCTCCTTTAAC TCATCTCGAATCTCTCTCATACAT
6967	Table 1	NA	466H5	-1	CTCTTATCCTGCTCTGCCCTGGAACT TGAACCCCAGTGCCAATACTCATG
6968	Table 1	NA	466B7	-1	CGACCTAATCTCTGTCCCCAGAAGGC AGACCAGGACTCCAGCCCCAGGAG
6969	Table 2	NA	466B10	-1	GCCAAATCTTTGTCCTGTACAAAGTA CAGATGTTTTTGACTGAAGTTCCA
6970	Table 1	NA	466C9	-1	GCCACAGTGAATAAATACAAGGCAAG GCTCATAGGTAAAACAAGTTCTAT
6971	Table 1	Hs.7187	mRNA for KIAA1757 protein, partial cds /cds=(347,4576)	-1	AGTGGAGTGTTTACACCTTGCTGTAA CATTTGAACTTTCACAAGAGATGT
6972	Table 1	NA	121F1 .	-1	AAACCCACCCATCATTTGCCCTGACT ACCCATCTCCCGATTAATTCACCC
6973	Table 1	NA	121A11	-1	AGGGAACAGAGCCAGGATTTAAACTC TAACAATTTGTCTCCACAATTGCA
6974	Table 3A	NA	121F8	-1	CTCCTGGCACGACAGAACTAGTAGTT TCCATGTCTTGAGGACATAGGTCC
6975	Table 1	NA	178B2	-1	TCGAACCTGTTCCAGGTATGCTGATA GATGTCGGTAGGGCATCCTTAATT
6976	Table 3A	NA	178B5	-1	GAGGTACTATAAACCAGATGCCCAAA ACACCTGCCCTCCTGGGTTGGCCG
6977	Table 1	NA	178F5	-1	ACATTCATCTGTTTCCACTGAGGTCT GAGTCTTCAAGTTTTCACCCCAGC
6978	Table 1	NA	178C12	-1	TTAGCCCTTTTCTGCGCTAATTAGAAT TTCAAGCGTCACAGAGCCTGGGG
6979	Table 1	NA	462A11	-1	TTCAACGAGGTGAACCAGTGTGATGT CTGTGGGGAAAACACGTAGTCAGG
6980	Table 1	Hs.13231	od15d12.s1 cDNA	-1	GGAAAAAGAAATTTCCTGAGATTTC
6981	Table 1	NA	/clone=IMAGE:1368023 462D9	-1	CAGTGTATACAGAAGTGTCTTTCCAT GAGTTCACGTGGGGTGGCCCTCCTC AGTGCTCTTAGGGTACTGTACT
6982	Table 1	NA .	462E8	-1	CCACCTTCGAGGTCCCTTCCGGCCTA AGATGCCTGAAATCTCCAAGGAAA
6983	Table 1	NA	462F9	-1	ACAAGGCAAAGCTTAAAGAAACACTA AACGAATGAGTGAAAGAAGCGGAG
6984	Table 1	NA	462F11	-1	TTCTCAATAACAAACCCAGGGCTTTC ATAAATGCATGATCAAAATGTGGA
6985	Table 1	NA	462G12	-1	ACAGAAAATAGGGTGTATATCAGCAT. TACGCTGATTCAGCAGAAGATAGC
6986	Table 1	NA	462H9	-1	TCTCGACTGACACCCACTATAAATTC CCTGGGTTGAAAAACTTTTCTTTT
6987	Table 1	NA	472B1	-1	TCCAAACCCCTCCATTACAATCTAAC ACACTTCCCCCTACATCGTCTCCT
6988	Table 1	NA	472C1	-1	GCATTTATTTTCTTCTACAGAGAACCT GGCGGCTGGGTCTGGGAAAGAGC
6989	Table 1	NA	472E6	-1	ACCCACAATTAGTGAGAGTGCCCTTG AGCTTGAGATTCCCATTCCTCCTT
6990	Table 1	NA	472F4	-1	TGGATATAAAGTGTGTGTTCTGACAG AAAATGGGGAGAAGGTGGCTATTT
6991	Table 1	NA	472G2	-1	GCCAGAAAATCCTGGTTTCCCTGGTG TCCCCTCCAATCTCTTTTACCAAA
6992	Table 1	NA	472D7	-1	CCATTGTCGCCCGGAGCTGGAAAGA TAGTTTAGAGAATGCCTTAGCACTT
6993	Table 1	NA	472G12	-1	CAGCACCCAGTACAGGTATGCAGGA AGGACTCGCTTGACTTAGAGAGTGG

			Table 8		
6994	Table 1	Hs.75354	mRNA for KIAA0219 gene, partial cds /cds=(0,7239)	-1	AACACACCAGAAGGAAAAGACACAGA CAGGGAATGAAGCCTGCAAAGTCC
6995	Table 2	NA	64G9	-1	GTAACTCAGTGCCCCCAAAGATTCAT
6996	Table 1	NA	467E5	-1	AGTCAGCAGGATTGGCCAGCAAAT CGCCCCAAATATAAAATCTCAATACC
6997	Table 1	NA	467A8	-1	AGTTCCTTTTCCCCAGTACCCCAG AGTCACAGGATGTTCTCTGCACCTCA
6998	Table 1	NA	467C9	-1	TCTGCAACTCTGAGCCTTACTCAA GTTAGAGCCCTCGTGCCCTGCTTCTT
6999	Table 3A	NA .	467F8	-1	CAGCTACCATTTCTCTCTGTGACC CCACCACAACCACACACACAAAAAGT
7000	Table 1	NA .	468E6	-1	CAACCCACACGAATATACCGGAAA CAGTTGGGCTGTTAGTAGTCTGTCAC
					ACAGGTGAGAGGAGCAAGAGATCC
7001	Table 1	NA	468B9	-1	AATCTATTATCAGGCATTTAATCACTG AGCACTCTTCTGTCCCACACTGT
7002	Table 1	NA	468E10	-1	AGAGGAGTGACGGTGAATGGTACTG AAAGCGGTTGTAAATTGCGAGAGAG
7003	Table 1	NA ·	468F10	-1	TCTCCTTGTTCTGATTCTCTCCCCATC TACAACAACTCCACTCC
7004	Table 1	NA	468F11	-1	CACCTAACCAAGCGGGTTGGGCTGA TGACCGATGACCGTAAGCAGTAAGG
7005	Table 1	NA	468G12	-1	ACCTCTTCTTTAGCAACACTAACCAC TCCACACTGGGGAAATTATACTCT
7006	Table 1	NA	468H11	-1	ACTACCGCACAACAGAACACATGACC
7007	Table 1	NA	469B6	-1	AGGTGAGTGCAGACACGACATCAG CAGTTTTACTCCTGGTCATCTCTTGT
7008	Table 1	NA	469D2	-1	GAGTGTGGATTCTTCTCTGCCCCT TTTTATTTTGGCTGAAGTTTGGGTATG
7009	Table 1	NA	469A10	-1	GCTGCTTGTTGGCCTCTGCTGGG ACAGCTTATAAAGCACTTTCTCATGC
7010	Table 1	NA	469E12	-1	ACTTCTTCTCGCCGTATTTGCACA GGGGCTCAAACCTGTGACTTACTGCT
7011	Table 1	NA	469F8	-1	AACTAACATCAAAGGAAAAGCTGG ATGATCATTGATAGATATTCTAAGAG
	Table 1	NA .	469G8	-1	CATGCAGGAATGAGGATGCGTGCC GACAACAAACCTGCTTGCTTGGTTAC
	Table 1	NA .	470B2	-1	CCACAGCGCACTGAGTATAGAAGT TCTTCAATTATTCATGCTCTAAGGCA
				-1	GTGTCTGTCTTCCCACCATCCCGC
	Table 1	Hs.118174	tetratricopeptide repeat domain 3 (TTC3), mRNA /cds=(2082,7480)		TGAGTATTTTTAAAATCCCCTGTTTGG ATGCTTCCAGCTAAATAGTCTACCT
	Table 1	NA	470C3	-1	TGGGTTTACTCAGATCTTCTCCTTCTT AAGTGAGAGTTTTAACCTACATTTT
7018	Table 1	NA ·	470D5	-1	GTCCAGAGCTAGAAGAACCAAGTCTT CCTTTCTTCATTCATTGTTCAGGT
7017	Table 1	NA	470E1	-1	CTTCTTCTTAGGATCTGGAGGGAGGG GAGTGTTAGAGCTTGTGAGCCATG
7018	Table 1	NA	470E5	-1	CTGAACGAACCAGTTCTTTTGGACTA CCAGTTCTTGAAGTGAAG
7019	Table 1	NA	470F3	-1	AACAAAAGCACTGACAAGCTCATATG AACAGGCTAAAAAGTGAGTGAAGT
7020	Table 1	NA	470G6	-1	TTCTCTTTCTATATCTAGCTAAATTGC CTGTGCGCCTCCCATCCTCCTCA
7021	Table 1	NA	470B8	-1	ACACACTTGATAAATTAGACCGATGC
7022	Table 1	NA	470G10	-1	AAACCGCAAGAATCCAAATCAGCT ATAGTAGGTGAGCCAGTAGTGTGAAT
7023	Table 1	NA	471D6	-1	GCTTGTCAAGCTTCCAAGGATGGA AACCACCACCCAGCTTCCTGGTACAA
7024	Table 1	NA	471F1	-1	GCAGGGACTCTGGCTACAGTGCTA TTTCCTCCCCTCCCTCCCCAATCCAC
7025	Table 1	NA	471F4	-1	AAAACACGTAATTCTGACTATCCA CAACATTCACAAAACTGGTCCCCGAA
7026	Table 1	NA .	471F6	-1	TTAGTGAGAAGGTTCCAGGAGTGC GAGAGATTATAGCACAGTCTCCCAGG
7027	Table 1	NA .	471E9	-1	GCTCAGTCAGGTCATCCGCAGCAA TTCAATGCTTTGTCCTCCCCTCGCAG
7028	Table 1	NA .	471E11	-1	ATGTTTAGAACAGATCCTCCTTCT
7028		NA .			TCCCTCTCTCAGGGCTGGGAAAGAAA GGTTCATCTTCACTCAGATGCAAG TTCTGTTGGTCTGCCAGCTCATCCAT
	Table 1	•••	471H11	-1	TCATCCATCACCTGCCAGCTAGAC
7030	Table 1	NA	473E4	-1	ACACAGTTTTGGCTCCCTTATTTTCC CCGTACTCGAAACATTTCCATGCA
7031	Table 1	NA	473F3	-1	ACCAAATCGCAAAAATACAGAATGCC TGTAAATTGAGTCACACCTTAAAA
	Table 1	NA	473E11	-1	GAGTCCATAAATCTGCATTTCATGTA GTTGTAAGACTTTCTCCCAAAGGT
7033	Table 1	NA	476C1	-1	TCCATTTGAGTTTTCTCCCATCTCTC ACAGTTGATTGTTCTGTCCCTTC

			Table 8		
7034	Table 1	NA	476D3	-1	AAAATTCAGCCCTCCTGGATTCACGT
7035	Table 1	NA	476F5	-1	GCCCAATGAAAGTCCCCAAACTAG TTTAACAGGAAAAGCCCAAAATTATTT
7036	Table 1	NA	476G3	-1	TTATGCTGTCTACAATCTGGGCC AGTTGCACTGGTTGTTCTTGGCTGCG
7037	Table 2	NA	476G4	-1	GTGCTTCTCACACAAGAAGCCCAG TTTCCTTTTTCCCTTGTCCCTTGGCTT
7038	Table 1	NA	476A10	-1	CCCCCATCACCGAATCCCCCTTC CTCCCACGCCTGGCCGTAGTCCAGA
7039	Table 1	NA	476G8	-1	GCTTCTTCTTTTTCATGGTTGGGTT GCCAGTGTACGTTGCCAGGCATTTCA
7040	Table 1	NA	476H10	-1	TGTAAGAGAAAACTCAAATAGCCA CCGTCTTCTTTTGGGTGTTTCCTCCT
7041	Table 2	NA	477E1	-1	AGTTTCGGCGGAAATCAGAGTTCA ATGAACCCTCACCTGCTCTGCAGTGC
7042	Table 1	NA	477E6	-1	AGTTTTGATTTTAGTCCCAGCAAA AGATATAGATGGTAAAATGTGATGCA
					ATGTAAAAAAATGGTAATACACACAC TCTCCA
	Table 2	NA	477A11	-1	TGAGTGGGCTTCTCTTATGGTACAGT CTCTTCTCTATGAGGGGCTTCAAA
	Table 1	NA	477D9	-1	TGGGCTTCCAAATGGTACAATGGAGT AATCAAGCTCATGGACTGAGAGTT
	Table 1	NA	477D10	-1	CTTGAAGCTACTTGTCCCTTTCTGTG CCAGACCACTTAATGGCTACCCAC
	Table 2	NA	480A3	-1	TTCCCAGGGCGCTCCATCTACAGCCT TACTGTGACTCCACTCAGCACCAG
	Table 1	NA	480B5	-1	ATTCCCCCTAAGCTCCTGTCCCCCGC CATGCACGACTGGTCACATCAAAA
	Table 1	NA	480D2	-1	AAGACACACCCCTCCTGTTTAATAAA AGTTGTCCCCTCGACATGCATAAT
	Table 1	NA	480E2	-1	CCTGGTTACAATAATGAAACTGTCGT GGAGTAAAGAGGGAAACATGACCA
	Table 1	NA	480E3	-1	AGAACCCACACACTGGGAGACAATAA CTGCCATTCATATAACCAACAGAA
7051		NA	480F3	-1	CGCCACTGCTTAAAGATTACAGACAA TTCCCAGGTAAAGTTGCCAGGACT
	Table 1	NA	480G4	-1	ACAATGATGTTTGAAACGCACTCTGA ATCTGTGAAAGCTAGATAAGTCCT
	Table 1	NA	480C8	-1	GCCTTCCTCCTCCTCCTCTTTGGGCC TATGTCCTAGATAAGCCTGTTAAA
7054	Table 1	NA	480D9	-1	TGTCAAGATGACAGATCTTAATCCAG AGTGGAGGCTCGTTCGGCCTGGAG
	Table 1	NA	480E7	-1	TTTATGTTTCAGCCTCTTTCTCTCCCG TTGAGTCCTGCCACAAGTCCTGC
	Table 1	NA	480E11	-1	ATTGTCCAGGTGACTTGACACTTGCC TACCGGAAAAGTTGGGATGTTCTT
7057	Table 1	NA	480F8	-1	TAAAATATGCCCTAATTTAAAGGGCG CAGGGTCCCACAACAAGCCACAGA
7058	Table 1	· NA	487F11 499G1	-1	AAATCTCTTCTCACGTTCTGTTTGTCA TTTAATCACCAGGTTTTTTAGCGC
7060	Table 3A Table 1	NA ·	518F10	-1	GCTACTGATGGGTGGCCCTTTATTCT TGTCTTTATTTGTTGTGTGCAGGA AAAAATTGGTAGCTGCCCCCATGTGG
7060	Table 1	NA:	524A12	-1	TATGATGTTTAATTTGAACAACAT ACCCGGCACGTCTCCTCAACCCCTTA
7062	Table 1	NA .	526B9	-1	ATTCTTTTCCAGCTTTTCATATTA CTCAAGAGGGCATAGACATTCCACAC
7063	Table 1	NA .	583B5	-1	GAGGACTGCATTCGTCAGGGTAAC AACAAATACCCAATTAACTGTATTCCC
7064	Table 1	NA ·	583D6	-1	CTTTCCCCTATGACTGCTGGTGT CCGTTGTCCGAAAGCTTGCTTCCAAC
7065	Table 1	NA .	583G8	-1	TAAAGACCAGAGATGGGAGGGAGT TTTAGCCCAAAGAAGACTTTCGCATA
7066	Table 3A	NA ·	584A1	-1	AATTCTGCCGTAACCCTTGTTGGA CAAAGCAGCAAATACAGAGCACACAA
7067	Table 1	NA	584D3	-1	CAATCCTTGGCCTGAGCAGAACAA ATATGAAGATGGATTGGAT
7068	Table 3A	NA	DNA sequence from clone RP4-620E11 on chromosome 20q11.2-12 Contains t	-1	GACAAAACGAAGACATGCCGGGCC ATGCCTAGTCAGTCAGTATTTCTTCTT GCTGCAGGTGTCTAAAAACCCAC
7069	Table 3A	NA	591H9	-1	CCTTCGCATTCCCCCATCCATGCTCC AAGATAATAGATTTTTCTTTAAAA

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			Table 8		
7070	Table 3A	Hs.6179	DNA sequence from done RP3-434P1 on chromosome 2C Oralians he KCNLN gene for inventily redifying polassium channel. M flippocampal inward rediffer, HRI, HRKH, HRKV2, KRZ-3, the KDRLR3 gene for KDEL (Iys-Asp-Glu-Leu) endoplasmic redictulum prolein relention receptor 3, the DDXf7 gene for DEADH (Asp-Glu-Leu) Aspfilish box polyperight of 17(28D), ESTs, STSs, GSSs and six putalive Cop listands federalor 27(28D)	-1	GGGGAACACTTTGGTTTGAAAGCACA GAGCAGTTTGCCATGTTTCTTCTG
7071	Table 1	Hs.44577	602388170F1 cDNA, 5' end /clone=IMAGE:4517129 /clone_end=5'	-1	ACTGAATGGTCGAAATCACATATGCA CCACACATACTGATCTTAAGTAAC
7072	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026	-1	CGAGGTACAGCAAAGCGACCCTTGG
7073	Table 1	NA	/cds=UNKNOWN 119F12	-1	TGTCATAGATCAGACGGAAATTCTC TACAGAAGAGCAGAGACCAACCTTCT CAAAGTTGGTGAGTATTAACCCAG
7074	Table 1	NA	119G10	-1	CCAGATTTGCTGATGTGTTAGGTAGT TGTGGCACACTCACCTGTCTTTCC
7075	Table 1	NA	485A6	-1	CTTTCCAGGTTTTCCCTTTCCGCCAT
7076	Table 1	NA	485D5	-1	TGTTTTCCCGCTCGCTAAAGTGAC TTGAACATTCGCAAAGTAACATCTCT CACTCCCAACACCACAGCTTATCG
7077	Table 1	NA	489H9	-1	AGTAACCACCAAAGCATAGTTTTAGA
7078	Table 2	NA	494B11	-1	AGGGCTTTCGCAAACCTAGCCTTT TCTTGCTTGTTCTTCTCGTTTTTGTTT TATCTTCCGCCCGGCAGGGTCAG
7079	Table 1	NA .	478E5	-1	GCTCTGAAACCCCTGGAACTCTTGAG CCTAAAATGTATTTTTTACAATCTT
7080	Table 1	NA	478G6	-1	ATCTTTGATGTGAAGCCCTTTAAAAAT AAACGTGAAGGTGCCAGCTTGCA
7081	Table 3A	NA	478H3	-1	ACCCAGCCTGATGTTCATCTTTTCCC CCTCTTCATTTTCCTTCTTTGTTT
7082	Table 1	NA	478C7	-1	AGAAAGACTAACACCAGAAATCATGC TGCAACACCAGAACATCCTTTGGA
7083	Table 1	NA	478G8	-1	TCACAAAATATGGCTCAAGGAGTATA AATCCCCTCTCACGCACCACAAA
7084	Table 1	NA	478H7	-1	ACTAACCAACCAATGAGAATACTACT TACCTCCACCCATGCTGTGAACCC
7085	Table 3A	NA	479B4	-1	TGACCGCCTCAAAGACCAAAAGGACT CTACTCCATATTCTTCTCACTGTC
7086	Table 1	NA	479D2	-1	GAATGACCACCTGACGCATTCAGAGC TCACCTTCTTGTTCTTCAGCTGTT
7087	Table 1	NA	479G2	-1	TTGGTAGAAACCACCCAACCATAAAA TTCCCAAGCCTGTACTGGTCAGCC
7088	Table 1	NA ·	479G3	-1	CATAAGTTGGGTGAAGAAATGGTGGT TTTAATCAGTAATATAGCTCCCCC
7089	Table 1	NA	479G5	-1	TTCTCATCTCAATATCCCCCAGAGCC CCAGTACCTCATAATACAAGACTT
7090	Table 1	NA	479G6	-1	CTATCAGGCCCTCCAGATAGTCTTCT ATAAACCAATGATTCAGCAGGACT
7091	Table 1	NA	479H4	-1	TACCCAAAGTCTATTCGTAAGTGCAT CTTTTCTATTAGACTGGAAGCTCC
7092	Table 1	NA	479H5	-1	GATGGTTCAGCAACTGAGGAGCTCA GGGTGACGGGTCCACAGAGCACAGA
7093	Table 1	NA	479H6	-1	AGAAATTAGAAGATGACTACCATTTG CTAAAGTCTATCCACATGCCAGCA
7094	Table 1	NA	479G12	-1	CCCCCTCGACCCCCTCACACCCTTTC CAGAGAGGCCTTAAGATTCCCATT
7095	Table 1	NA	479H12	-1	TGTAAGGTTTCATAAATTTAGAGACC CTAGCCAGTCAGTGACAATATGCA
7096	Table 1	NA	482A5	-1	GAGTTGCTTATTCCAGTCTCTCTAAG ATATATCTCCCTTTTTAGTTGCTGAC
7097	Table 3A	NA	483G5	-1	TGGTGTAATGAACATGCCGTATTGCC TTTATGGCCAGTTTGAGTCCTTCC
7098	Table 1	NA	486C4	-1	AGGGAACCCCAAAGAGTTAAAACCAG GACCACTATTTCATAGTCAACAAA
7099	Table 1	NA	490F10	-1	GTGGTAAATGAGAGCATTACAGACCA CCCACATCAGCCTAAAATATAATT
7100	Table 1	NA.	493C2	-1	CCACCAAACCCAACAGGCCGGGACA AATGCAATACCATACAGAAACACAG

 GGCCAAACTTTCTTACTCTGCCATTT GTTCAATGTCCTAATGAGCATGAA DNA sequence from PAC 66H14 on chromosome 6q21-22. Contains FYN (P59-FYN, SYN, SLK) gene coding for two isoforms. Contains ESTs and STSs (cde-147-470e). ATCAATCGGGCCAATCCGAAGTCAGC AATCTTGCATATGAGTCCATTCCC

58G4

7101 Table 1

7102 Table 3A

NA

Hs.169370

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					Table 8		
7103	Table 1	NA			598H2	-1	TATTTTTAACAAAATCACACGGAAGG
7104	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10,	-1	ATTTCCTTCCCGTCCCATGTGTTG CAGATAGTGGTATTTGGGTGCTGGG CTTGTCTGACCTGAGGAGGTGGCTG
7105	Table 3A	NA	AA501725	2236692	mRNA sequence ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element, mRNA	-1	AACTCCATAGAGAAAGACTACGAATT TCGCTGGGAGGTAATAGGGAAGCC
7106	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	-1	GCATTTAGGAAAGACAGGTGAGTGTG CCACAACTACCTAACACATCAGCA
7107	Table 3A	NA	AA579400	2357584	nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915561 similar to contains Alu repetitive element;contains	-1	TTACTTTGTCTTCTCTCACCATCCTAA AACGTTGTTTTGCTGAGCATGAA
7108	Table 3A	NA	AF249845	8099620	isolate Siddi 10 hypervariable region I, mitochondrial sequence	-1	CCCCAGACGAAAATACCAAATGCATG GAGAGCTCCCGTGAGTGGTTAATA
7109	db mining	Hs.277051	Al630242	4681572	ad07c09.y1 cDNA /clone=ad07c09- (random)	-1	GCCTAAGTTTCCAGAAGACTTTGACG ATGGAGAGCATGCAAAGCAGGTAA
7110	db mining	Hs.277052	Al630342	4681672	ad08g11.y1 cDNA /clone=ad08g11- (random)	-1	TTTTGCAGTTCAAGGATTGGTGGGAA ACGTTTGTATGTGTTGGGGTGGGG
7111	db mining	NA	Al732228	5053341	nf19e05,x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element;, mRNA s	-1	AATAGATTTCCATTTCTTCCTTCGAGT TAGTTGGGTATTGGGACCTTGAA
7112	Table 3A	NA	AW379049	6883708	RC3-HT0230-201199-013-c12 HT0230 cDNA, mRNA sequence	-1	CGACGGTGTTCTGGAGTTTCGATGAG ACATGTAAGTAAGAGTTCTGTGCA
7113	Table 3A	Hs.232000	AW380881	6885540	UI-H-Bi0p-abh-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3'	-1	ATATTCAGCAGTGGCTGTGAAATTGG ATTTGAATTACCGGGATACATGCA
7114	Table 3A	Hs.325568	AW384988	6889647	602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	-1	ACTGGTTTTCATTCTAGTGTCCCCCA CCCGTCTAGTTTCATTTTCCTGTA
7115	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	-1	TTGGGAGTCACCAGGTTAAAGCAAAG CCTCAGTCACTGAAAGCAGAAACT
7116	Table 3A	NA	AW837717	7931691	CM2-LT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	-1	TCCTGTGCTCCAGAATTAGTGATTGC TTTGGTGCTTAACTTGAAGTGGGA
7117	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	-1	CATCTGCTCTGCTTCCTCACACACTA GAAACACCACTGCCCCCATCCATG
7118	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	-1	TCTGTGATTTATAGACTGTTTTCAGGA AACGATCTTCCCATCTGTGGTGA
7119	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	-1	TCATTTCAGGTCTAATAAACACACTAA CCTCGGCAGCACTGGAGCGTCTG
7120	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	-1	AGCTTAGGATATCTATTAGTGTTCACT GTTCGGGCAAGAGGCCTAAAGGG
7121	Table 3A	NA .	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	-1	TGGGAACACACTGGCCCATTATATAG AGAAAAATAAAACATGATCCCCAT
7122	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041 cDNA, mRNA sequence	-1	TTGCTTGATTTCCCAAACCACTACCT GAAGGTGGCTTATGGTCTACAGCT
7123	Table 3A	NA	BE086078	8478469	PM2-BT0672-130400-006-h09 BT0672 cDNA, mRNA sequence	-1	TTCCACCACTTCAAGACTGGGGGCA GGTAGAGAAGACAAGCATAAGTACA
7124	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	-1	TTCTTCTCTGCCCCCTAACAGAATGTT CTTCTCTTGCTTCCCACACCCTCC
7125	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	-1	CAGCACATCTTCTGGTTTACAAGTTG GGTAACTATGAAAGCTGGAGATGC
7126	Table 3A	NA	BE163108	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	-1	TATCTAAATTCTACCTTTAGCATCCAA CTAGCTACCGTCTGGCACTGGCC
7127	Table 3A	Hs.301497	BE168334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	-1	TCCAATGCTCAAGTCACTCTGAGTCT TTGCTGGTGTCAACCTACAATGCC
7128	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	-1	ACCTCACTATAGTAGCCATTAGGTAA AGATGGGCCATATCCAAATGGGCT
7129	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	-1	AAGAACTATTCCTTTGAGAATCTTTCC TACTGGGAGTTACTGCTGTGATT
7130	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	-1	TCTGTGTGAACATACATACAGGACTT TGATTCTACCTGTGCCTGACCATT
7131	Table 3A	NA	BE247056	9098807	TCBAP1D6404 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-	-1	GTGGAGCTGTTGGCCTTGCTGGATG CGGGCACTCTCTACACCTTCAGGTA
7132	Table 3A	Hs.11050	BE763412	10193336	HGSC project=TCBA cDNA clone T mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	-1	TGTCAGTGGCTCTCACTTTGTTTGAA ATTGTTGCTTTGGGAAAAACACAG
7133	Table 3A	NA	BF330908	11301656	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	-1	GATGCAGTGGGTTAGGGGTTGGGGG TACAGACTGACTTGAGCTCGGAGTC
7134	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	-1	TCAGGCACTCAGTAAAGGCAAGACTT GAGTGATACATAAAGTCAGTTACA
7135	Table 3A	NA	BF364413	11326438	RC6-NN1068-070600-011-801 NN1068 cDNA, mRNA sequence	-1	CCTTGGGCTGAGTTTGCTGGTCCTGA AGATTACAGTTTTGGTTAGAGAGA

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						Table 8		
71	36	Table 3A	NA	BF373638	11335663	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	-1	ACAGCAAACAAAGTGTTCCAATCCTC TATTAACCCATTTAACCAAGAGTT
71	37	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	-1	AGTGCATTCACACTGATGATAAACGA TAGTAGCTTCACAGGTTTGCTTCT
71	38	Table 3A	NA	BF749089	12075765	MR2-BN0386-051000-014-b04 BN0386 cDNA, mRNA sequence	-1	AAGTGTGATTAGAAGCAGCTGGAAGT AGCAGAGGAGGTGGAAGTTAGTCC
71	39	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	-1	CAGGAGTAAAACAGAGCTGGTTGTGT GATACCTATGCTGGGTGGAAGACT
71	40	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	-1	GGTGACTATCTTACCGGCTCCCAGTA AACTCTGAACAATGTACCAGCTAA
71	41	Table 3A	NA	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	-1	GCTTGAAGATGTCTCAACAGAAAATC ACCGACATGAGGAAGCATCACGCT
71	42	Table 3A	NA	BF805164	12134153	QV1-Cl0173-061100-456-f03 Cl0173 cDNA, mRNA sequence	-1	AGGAACATGGCTGCAGCATATAAAAA GAATTGAATTCCATACTTTTGTTAACC
71	43	Table 3A	NA	BF818594	12156027	MR3-Cl0184-201200-009-a04 Cl0184 cDNA, mRNA sequence	-1	GGTGCTGCCATAGGTGCCAGTAATG ACCGTTTATGCGGAAATCAATTACA
71	44	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	-1	TGAAGTACTATAGGACTCAATGGGAC CAGTAGCAGCTCCAAGTGGATCAC
71	45	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	-1	ACACGGGACCTCCTTTGATCTTTCTG AGAATTAATAGAGATTTCATGGCA
71	46	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	-1	CCAAAAGGAGAAAGATGACTAGGGT CACACTTGAGGATTTGCCAGGTGGG
71	47	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	-1	GCATCTTCTTTGAAGACGGGAACTGT ACTTCAGGTTCTTTTCTGTTTAGC
71	48	Table 3A	NA	BF877979	12268109	MR0-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	-1	GGCTCATTTGGTTTTAAAGTCTCTTCT ATGCCATCCCAGGGGAGGAGGAT
71	49	Table 3A	NA	BF897042	12286501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	-1	GACTGTGGACACCTCTCACTGTGTCT TCTTGGCAGGCAGAGCTTACTGAC
71	50	Table 3A	NA	BF698285	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	4	GCAGGGTGCAGAGCTTCACAGCAGG TAGGAAGAAGTAACTAAGTGGAAAC
71	51	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	-1	CAGCTAAAGCCGTAGGTCATTGTGAC TGTCCCTGGGATGTGGATTACTCT
71	52	Table 3A	NA	BF904425	12295884	CM1-MT0245-211200-662-d02 MT0245 cDNA, mRNA sequence	-1	CCAGAATGCAGCCTACAGACCAAATA TCAATGGACTTGGTGTAGCCCTGC
71	53	Table 3A	NA .	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	-1	TTTAAACCAGGTCTGGAAAAAGGAAG GAGAGGAGGCATTTTAGAGAAGA
71	54	Table 3A	NA	BF926167	12323197	CM2-NT0193-301100-562-c07 NT0193 cDNA, mRNA sequence	-1	GTGGCTTCGTAAAATAGAAGAGCAGT CACTGTGGAACTACCAAATGGCGA
71	55	Table 3A	NA	BF928844	12326772	QV3-NT0216-061200-517-g03 NT0216 cDNA, mRNA sequence	-1	CACACCACAGCTGGCTGGGAGCAGA GGCTGCTGGTCTCATAGTAATCTAC
71	56	Table 3A	NA	BG008620	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	-1	TGGAGAAATGAGAGACAGACAGTG AGTGAGAAAGTCAGCGAAAAGGAAA
71	57	Table 3A	NA	F11941	706260	HSC33F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	-1	ACCTACTGTTGAGATTATTCCCCTGT CTCCACACTGCCAGAAACTTACCA
71	58	Table 3A	NA	U46388	1236904	HSU46368 Human pancreatic cancer cell line Patu 8986t cDNA clone xs425, mRNA sequence	-1	CCAAATGATACTAGGATTAAGCCCCA AAGCAAAGTCAAGCACCACCATGG
71	59	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	-1	TCCCAGAGCAACAACTAAGTCTCAAC TAATGGACAACCAACACCCACTGA
71	60	Table 3A	NA	W27656	1307658	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	-1	CCACAGAATGGGCATGTAGTATTGAG ATTTGAATCATCTGCTGTCCAGCC
71	61	db mining	Hs.681	NM_004146	10764846	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18) (NDUFB7), mRNA /cds=(22,435)	1	ACCTCATCCGGCTGCTCAAGTGCAAG CGTGACAGCTTCCCCAACTTCCTG
71	62	db mining	Hs.943	NM_004221	4758811	natural killer cell transcript 4 (NK4), mRNA /cds=(59,763)	. 1	GACCTGGTGCTGTCGCCCTGGCATC TTAATAAAACCTGCTTATACTTCCC
71	63	db mining	Hs.1063	NM_003093	4507126	small nuclear ribonucleoprotein polypeptide C (SNRPC), mRNA /cds=(15,494)	1	GCATAAGGAAGACTTGCTCCCCTGTC CTATGAAAGAGAATAGTTTTGGAG
71	64	db mining	Hs.1321	NM_000505	9961354	coagulation factor XII (Hageman factor) (F12), mRNA /cds=(49,1896)	1	GGGACTCATCTTTCCCTCCTTGGTGA TTCCGCAGTGAGAGAGTGGCTGGG
71	65	db mining	Hs.288856	NM_003903	14110370	prefoldin 5 (PFDN5), mRNA /cds=(423,926)	1	AGACTGGATCGCACACCTTTGCAACA GATGTGTTCTGATTCTCTGAACCT
71	66	db mining	Hs.1975	NM_030794	13540575	hypothetical protein FLJ21007 (FLJ21007), mRNA /cds=(257,2212)	. 1	AAGCAAATACCTTTTACAAGTGAAAG GAAGAATTTTTCTTCTGCCGTCAA
71	67	db mining	Hs.3804	NM_014045	13027587	DKFZP564C1940 protein (DKFZP564C1940), mRNA /cds=(565,1280)	1	GCAACAAATGCTTCTATTCCATAGCT ACGGCATTGCTCAGTAAGTTGAGG
71	68	db mining	Hs.3832	NM_032493	14210503	clathrin-associated protein AP47 (AP47), mRNA /cds=(76,1347)	1	TCCGTGTAGAGGTTACAGCCTTTTAT GCTGTTGAGCTCCCAGGTACCAAA
71	69	db mining	Hs.4113	NM_006621	5729723	S-adenosylhomocystelne hydrolase- like 1 (AHCYL1), mRNA /cds=(47,1549)	1	GCCACTTGGATTTATAGTATAGCCC TTCCTCGACTCCCACCAGACTTGC
71	70	db mining	Hs.83848	NM_000991	13904865	triosephosphate isomerase 1 (TPH), mRNA /cds=(34,783)	1	AAGAGCTCCTGAGCCCCCTGCCCCC AGAGCAATAAAGTCAGCTGGCTTTC
71	71	db mining	Hs.5076	AK025781	10438401	cDNA: FLJ22128 fis, clone HEP19543 /cds=UNKNOWN	1	GCTCAACATGGAAAGAAGGTACAGAA AGTGATGTGTTCAAAACATTAGCA

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7172	db mining	Hs.5298	NM_015999	7705760	CGI-45 protein (LOC51094), mRNA	1	TTATATACCCTGGTCCCATCTTTCTAG
7173	db mining	Hs.5473	AW953785	8143468	/cds=(182,1294) 602659796F1 cDNA, 5' end /ctone=IMAGE:4802950 /ctone_end=5'	1	GGCCTGGATCTGCTTATAGAGCA GTTTACTCCGTCCCTATCACTGGTGT GGCTGTGGGCAAACCACTTATTGC
7174	db mining	Hs.5831	NM_003254	4507508	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1), mRNA	1	GAACTGAAGCCTGCACAGTGTCCAC CCTGTTCCCACTCCCATCTTTCTTC
7175	db mining	Hs.5890	BF698885	11984293	/cds=(62,685) hypothetical protein FLJ23306 (FLJ23306), mRNA /cds=(562,930)	1	GAAGACCAAGAGAGACAACAGACGC AGCAAACAGCCGAAGCACCAGACAA
7176	db mining	Hs.6211	NM_015846	7710138	methyl-CpG binding domain protein 1 (MBD1), transcript variant 1, mRNA	1	AATTCAGAAAATTGTTGGGAGGACAG CCCTTTTGTGAACCTTGTTTGGGG
7177	db mining	Hs.6285	AL080220	5262711	/cds=(139,1956) mRNA; cDNA DKFZp586P0123 (from clone DKFZp586P0123); partial cds	1	TTTACCCAGCTCTGAAGGTCATTGTT CTTGCCTGTGTTTGAATAAAATCA
7178	db mining	Hs.6441	AL110197	5817115	/cds=(0,1067) mRNA; cDNA DKFZp586J021 (from clone DKFZp586J021) /cds=UNKNOWN	1	GTCTCTGATGCTTTGTATCATTCTTGA GCAATCGCTCGGTCCGTGGACAA
7179	db mining	Hs.6459	NM_024531	13375681	hypothetical protein FLJ11856 (FLJ11856), mRNA /cds=(239,1578)	1	GGTAAGCCCCTGAGCCTGGGACCTA CATGTGGTTTGCGTAATAAAACATT
7180	db mining	Hs.6616	AL524742	12788235	AL524742 cDNA	1	TCTGGCTCTGACCGGTTGATGGCCTT
7181	db mining	Hs.6650	NM_007259	6005775	/clone=CS0DC008YI07-(5-prime) vacuolar protein sorting 45B (yeast homolog) (VPS45B), mRNA /cds=(33,1745)	1	GAGCGAATGAAATCATGAAATTGA TGCCCTACATAGCAATTTTCTGTGGC ACTGAGAAACCATGTATGACCACA
7182	db mining	Hs.6763	NM_015310	7662395	KIAA0942 protein (KIAA0942), mRNA	1	GCAGTGTACTGTGTGCAATACCAAGG
7183	db mining	Hs.6780	NM_007284	6005845	/cds=(52,1656) protein tyrosine kinase 9-like (A6- related protein) (PTK9L), mRNA /cds=(104,1153)	1	GCATAGCTCCCTGTAATTTGGGAA CTGAGACTAGGGTCCCAGCACAGCC CAGAAACCTTTGGCCACAAGAAGTG
7184	db mining	Hs.6817	NM_025200	13376793	putative oncogene protein hlc14-06-p	1	TCGCCTTCCATGGTTTTTAAATGCAG TAAATAACATTTCTGGATGAGACT
7185	db mining	Hs.7709	U79457	4205083	(HLC14-06-P), mRNA /cds=(51,635) Homo septens, Similar to WW domain binding protein 1, clone MGC:15305 IMAGE:4309279, mRNA, complete cds	1	GCTTTACCCCGCAGGACATACACAG GAGCCTTTGATCTCATTAAAGAGA
7186	db mining	Hs.7740	AF288741	14209837	/cds=(162,971) oxysterol binding protein 2 (OSBP2) mRNA, complete cds /cds=(112,2748)	1	GGAATGTACCTCTCCCCAACACTGTT TTGTTAGCGAGCACCTTTTGACCA
7187	db mining	Hs.8108	NM_021080	10835268	disabled (Drosophlla) homolog 1 (DAB1), mRNA /cds=(765,2426)	1	ACTCGCTCAGAAGAGGGAACTAAGC ATTTTTGGCAACCAATGGGCAGATA
7188	db mining	Hs.8109	NM_022743	12232400	hypothetical protein FLJ21080 (FLJ21080), mRNA /cds=(127,1236)	1	AGCTGTGTGAACCTCTCTTATTGGAA ATTCTGTTCCGTGTTTGTGTAGGT
7189	db mining	Hs.8207	NM_020198	9910241	GK001 protein (GK001), mRNA /cds=(184,1635)	1	AGTCCCATACATTTGGACCATGGCAG CTAATTTTGTAACTTAAGCATTCA
7190	db mining	Hs.226627	BC007375	13938462	leptin receptor short form (db) mRNA, complete cds /cds=(0,2690)	1	CTGCCCCCTTCCTGGACTTCGTGCCT TACTGAGTCTCTAAGACTTTTTCT
7191	db mining	Hs.8768	NM_018243	8922711	hypothetical protein FLJ10849 (FLJ10849), mRNA /cds=(93,1382)	1	GGATAACATTTCTCATGAACCCACTG CCCCTCTGCATTTTCCTCACTGGT
7192	db mining	Hs.8834	NM_006315	5454011	ring finger protein 3 (RNF3), mRNA /cds=(114,857)	1	CGCTTAAGAACATTGCCTCTGGGTGT CATGTGGACCAGACTTCTGAATAG
7193	db mining	Hs.9683	NM_006260	5453979	protein-knase, Interferon-inducible double stranded RNA dependent inhibitor (PRKRI), mRNA /cds=(890,2204)	1	GGGTTCAATCCCTTCAGCTCAGGCG GACCATTTAGATTTAAATTCCACTT
7194	db mining	Hs.9825	NM_016062	7706342	CGI-128 protein (LOC51647), mRNA /cds=(35,526)	1	GCTCCTGCCAGGGCTGTTACCGTTGT TTTCTTGAATCACTCACAATGAGA
7195	dis mining	Hs.10590	AL031685	9368423	DNA sequence from clone RPS- 963K23 on chromosome 20q13.11-13.2 Contains a KRT16 (Keratin type I, Cytoskeletal 18 (Cytokeratin 18, CK18,CYK18) pseudogene, a gene for a novel protein, the gene for spermatogenesis associated protein PD1 (KAA0757) and the 3' end of the gene for KIAA0393 (novel		AATCTGGCGAAACCTTCGTTTGAGGG ACTGATGTGAGTGTATGTCCACCT
7405		11- 4440-	NIA 004822	4758483	Sodium/hydrogen exchanger family member). Contains ESTs, STSs, GSSs and four putative CpG islands /cds=(2,688)		0.007.4.T0000000000000000000000000000000
7196	db mining	Hs.11465	NM_004832	4/58483	glutathione-S-transferase like; glutathione transferase omega (GSTTLp28), mRNA /cds=(9,734)	1	GACTATGGGCTCTGAAGGGGGCAGG AGTCAGCAATAAAGCTATGTCTGAT
7197	db mining	Hs.11538	NM_005720	5031600	actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1B), mRNA /cds=(80,1198)	1	AGGGAGGGGACAGATGGGGAGCTTT TCTTACCTATTCAAGGAATACGTGC

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7198	db mining	Hs.12707	AK023168	10434970	cDNA FLJ13106 fis, clone NT2RP3002455, highly similar to mRNA for KIAA0678 protein	1	ACCTTCTGAAAGCTCACAGTACACAT TAGTATGTATAACTGGCTTTACCA
7199	db mining	Hs.12785	AL031685	9368423	rodas–UNKNOVNI DNA sequence from clone RP5- BOSK23 on chromosome 20(13.11-13.2 Contains a NGT 10 (Pectatin by a L Contains a NGT 10 (Pectatin by a L CK 18(CVX 18)) pseudopene, a gene for a novel protein, the gene for spermatogenesia associated protein PDT (RCAND75) and the 3" end of the gene for KIA-OSS9 (howel Socialmyflyorigen exchange Tamily CK- CK 18(CVX 18) pseudopene exchange Tamily and the 3" end of the gene for KIA-OSS9 (howel Socialmyflyorigen exchange Tamily and Four putative Crypt (silands Code=Cq. 313)	1	TTTAAGGGAGTCAGGAATAGATGTAT GAACAGTGGTGTCACTGGATGCCT
7200	db mining	Hs.13323	NM_022752	12232416	hypothetical protein FLJ22059 (FLJ22059), mRNA /cds=(783,1967)	1	CCCACCTTCCACCTCTTAGCACTGGT GACCCCAAAAATGAAACCATCAAT
7201	db mining	Hs.13659	AL080209	5262698	Hypothetical protein DKFZp586F2423	1	AGACCAGCAGTGTTTAAATCTAAATA CGTTGTGAGTCTGTTATCTGTCCT
7202	db mining	Hs.14089	NM_013379	7019510	dipeptidyl peptidase 7 (DPP7), mRNA /cds=(0,1478)	1	ACCTCGACCTCAGAGCCTCCCACCC AGAAGATCCTGCTTCCGTGGTTGAG
7203	db mining	Hs.16488	NM_004343	5921996	calreticulin (CALR), mRNA /cds=(68,1321)	1	GGGCAGTGGGTCCCAGATTGGCTCA CACTGAGAATGTAAGAACTACAAAC
7204	db mining	Hs.16580	NM_018303	8922829	hypothetical protein FLJ11026 (FLJ11026), mRNA /cds=(31,2355)	1	TGGCCTTAAGTTTTCTAATTCAAGCG GGTTTTTGGAAAAATTTATGGTCT
7205	db mining	Hs.109438	AB028950	5689390	clone 24775 mRNA sequence /cds=UNKNOWN	1	TGCAGAGTTATAAGCCCCAAACAGGT CATGCTCCAATAAAAATGATTCTA
7206	db mining	Hs.18586	NM_014826		KIAA0451 gene product (KIAA0451), mRNA /cds=(1482,2219)	1	CCAAACAATGATGTGGATTCTTTTGC ACAGAAATATTTAAGGTGGGATGG
7207	db mining	Hs.19575	NM_015941	7706261	CGI-11 protein (LOC51608), mRNA /cds=(233,1684)	1	ACAAAAGTCAACTGTTGTCTCTTTTCA AACCAAATTGGGAGAATTGTTGC
7208	db mining	Hs.20529	AK025464		cDNA: FLJ21811 fis, clone HEP01037 /cds=UNKNOWN	1	GCTGGGGACTCTAGCCTCTGTGTTCA TAAAGACATTAAGAAGTGGATGGA
7209	db mining	Hs.20725	NM_020963	14211539	Mov10 (Moloney leukemia virus 10, mouse) homolog (MOV10), mRNA /cds=(70,3081)	1	GGAGAATGACACATCAAGCTGCTAAC AATTGGGGGAAGGGAA
7210	db mining	Hs.343590	AB011104	3043587	601471579F1 cDNA, 5' end /clone=IMAGE:3874747 /clone_end=5'	1	ACCTGGGTTTAATACAGCTCACATCA CTGAATGTTACACATGAGTTTAAA
7211	db mining	Hs.23449	NM_018842	10047119	insulIn receptor tyrosine kinase substrate (LOC55971), mRNA /cds=(333,1553)	1	CTTAAGGACGCCTTTGCCTGGCCCCT TTATTACAGCCCAACACGGTAGGC
7212	db mining	Hs.23990	NM_017838	8923443	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs) (NOLA2), mRNA /cds=(86,547)	1	TCCATCAGTGCCATTTCCTGTAGAAC TAAAGGCTGTTCCAAGAATGTGGG
7213	db mining	Hs.24024	NM_015376	7662333	KIAA0846 protein (KIAA0846), mRNA /cds=(272,2341)	1	ATCTGTAAAGCACTCAGAAGGCAGCC ATCCCTAGATGTTGGTTTCATGTA
7214	db mining	Hs.334842	BC008330	14249901	tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(67,1422)	1	TGGTTAGATTGTTTTCACTTGGTGAT CATGTCTTTTCCATGTGTACCTGT
7215	db mining	Hs.24641	AK022982	10434887	cDNA FLJ12920 fis, clone NT2RP2004594 /cds=(96,2144)	1	CATGTCCCTTGAAACATGATAGTTAC ATACACAGTTTTCTCTCCACACAT
7218	db mining	Hs.321105	NM_015462	7661683	cDNA; FLJ21737 fis, clone COLF3396 /cds=UNKNOWN	1	AGGTTTCACATGAACCTGTTCTAGGC TGTGGACATTGGTGTGGAGAGGTT
7217	db mining	Hs.26802	NM_021158	11058039	protein kinase domains containing protein similar to phosphoprotein C8FW (LOC57761), mRNA /cds=(294,1370)	1	GACACTTGGGGTCCACAATCCCAGG TCCATACTCTAGGTTTTGGATACCA
7218	db mining	Hs.26892	NM_018456	8922098	uncharacterized bone marrow protein BM040 (BM040), mRNA /cds=(357,749)	1	AGAAATGATTTGCAGCTGAGTGAATC AGGAAGTGACAGTGATGACTGAAG
7219	db mining	Hs.27076	NM_003729	4506588	RNA 3'-terminal phosphate cyclase (RPC), mRNA /cds=(170,1270)	1	TCCTGAGAGATGGACAATGAAATATC AGTTGGTGGATATGTGTGATAGCT
7220	db mining	Hs.27445	NM_016209	7706428	unknown (LOC51693), mRNA /cds=(58,480)	1	CTTTCAGGGCAGGCAGCTGTGCATG TTCTCTCAACTAAAGGTCTTGTGAG
7221	db mining	Hs.27633	NM_015456	7661663	DKFZP586B0519 protein (DKFZP586B0519), mRNA /cds=(75,1199)	1	GCTGGACACACGGTGAGATTTTCTCG TATGTAAATAAAAGGCAATTTGGT
7222	db mining	Hs.28310	BG260891	12770707	602372491F1 cDNA, 5' end /clone=IMAGE:4480510 /clone_end=5'	1	CTCAACGAAAGGCTCACACTAACAGG GGAGGATTACAGCACCACAATACT
7223	db mining	Hs.28914	NM_000485	4502170	adenine phosphoribosyltransferase (APRT), mRNA /cds=(71,613)	1	CCACACTGAACCCAATTACACACAGC GGGAGAACGCAGTAAACAGCTTTC
7224	db mining	Hs.29893	AL133426	6562628	mRNA full length insert cDNA clone EUROIMAGE 146397 /cds=UNKNOWN	1	AGGCCCTGGAAAATTTTGTGCTTCCA ACGTGGCCTTCAATTCTTGCTTTT
7225	db mining	Hs.30120	BF970066	12337281	602272333F1 cDNA, 5' end /clone=IMAGE:4360233 /clone_end=5'	1	TATTAAGCTTGCCCAGGGTCCTGTTC ATGAAGGTTCCCCCAGCGGTGGCC

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7226	db mining	Hs.30250	AF055376	3335147	short form transcription factor C-MAF (c-maf) mRNA, complete cds	1	GCTATACCACTGACTGTATTGAAAAC CAAAGTATTAAGAGGGGAAACGCC
7227	db mining	Hs.30443	AL136599	13276698	/cds=(807,1928) mRNA; cDNA DKFZp564G1816 (from clone DKFZp564G1816); complete cds	1	TCGGGGTCAGTTAAGCCTCAGTATTC TTAGCTTTTGTTGATTTTGGCACT
7228	db mining	Hs.31137	NM_006504	5729992	/cds=(137,3091) protein tyrosine phosphatase, receptor type, E (PTPRE), mRNA /cds=(51,2153)	1	ATGGTGCAAACCCTGGAACAGTATGA ATTCTGCTACAAAGTGGTACAAGA
7229	db mining	Hs.34114	NM_000702	4502270	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide (ATP1A2), mRNA	1	AGAAGCAGCGAGTGCATGGGCTAAT TATCATCAATCTTTATGTATTTGTT
7230	db mining	Hs.35254	NM_020119	9910221	/cds=(104,3166) hypothetical protein FLB6421 (FLB6421), mRNA /cds=(310,792)	1	GGAAATGTTGCTGTGGGGGATTCATT GTAACTCTCCTTGTGAACTGCTCA
7231	db mining	Hs.38735	BG149337	12661367	nad26g06.x1 cDNA, 3' end /clone=IMAGE:3366730 /clone_end=3'	1	ATGCCAAATTCCTGACACGTGGCGTT TGAAAATACCATGGAACGTTTCCA
7232	db mining	Hs.41322	Al655467	4739446	tt13b01.x1 cDNA, 3' end /clone=IMAGE:2240617 /clone_end=3'	1	ACATTCTGACTCCATCTGCGGCCTCA TTAAGGTGATAGAAACATACTAGG
7233	db mining	Hs.42346	AY013295	11693027	calcineurin-binding protein calsarcin-1 mRNA, complete cds /cds=(131,925)	1	ATGATAATGTTGGCATCTGTGATAAA CTATCAATGAGGCTCCCATCATGC
7234	db mining	Hs.42699	AW956580	8146278	EST368665 cDNA	1	AGAGTCACATGTAGAAAAGCCTCCAG TATTAAGCTCCTGAATTCATTCCT
7235	db mining	Hs.44131	AB023191	4589591	mRNA for KIAA0974 protein, partial	1	ATGGCAACAATGCTGACAGCAAGCA
7236	db mining	Hs.44441	BE295812	9179366	cds /cds=(0,1697) 601176827F1 cDNA, 5' end /clone=IMAGE:3532039 /clone_end=5'	1	GTAGATCCTCTGATTCCAATTACCA GGGAACCCTCATTAATTAGACAAGAA CACCAAGGCTATGACCACAGCAGC
7237	db mining	Hs.46919	AY007155	9956067	clone CDABP0095 mRNA sequence	1	GGCTCACCAGAGTACCCAGAAGAAT
7238	db mining	Hs.56009	NM_006187	5453823	/cds=UNKNOWN 2'-5'-oligoadenylate synthetase 3 (100 kD) (OAS3), mRNA /cds=(34,3297)	1	CAGTATGGAATTAGAGGACAGTGGC ATTCCAGGCCCTCAGTCTTTGGCAAT GGCCACCCTGGTGTTGGCATATTG
7239	db mining	Hs.57843	W63785	1371386	zd30g09.s1 cDNA, 3' end /clone=IMAGE:342208 /clone_end=3'	1	GCATACATAAAGGCAAAGAATGACAA AAGGCTTAATCCACCTAGAAGACA
7240	db mining	Hs.58373	BF339746	11286202	602034942F1 cDNA, 5' end /clone=IMAGE:4182851 /clone_end=5'	1	ATATAGTGGGAGACAAAACACAGGAG GCGGGGGATATCATGTAGCAGAGC
7241	db mining	Hs.59238	NM_032139	14149802	hypothetical protein DKFZp434L0718 (DKFZP434L0718), mRNA	1	TCTAATGTGCCTTGGATATGTGCCAA ATGATGGAAAAGAAACAGTAAACT
7242	db mining	Hs.82408	NM_024680	13375912	/cds=(133,3285) hypothetical protein FLJ22573 (FLJ22573), mRNA /cds=(99,1166)	1	GCTTGGCTCATCTGGGGTTTGCTGG GCTTAACACCCAATAAAGAACTTTG
7243	db mining	Hs.83042	NM_018457	8922156	DKFZp564J157 protein (DKFZP564J157), mRNA /cds=(77,523)	1	CTGCGGTTTTGGAACCTTACCTCTCC TCCTTAGCCCAATATGCTGTCTTG
7244	db mining	Hs.85848	NM_005105	4826971	RNA binding motif protein 8A	1	TCCAGGCCATTTTGCAGGGACTCTGA
7245	db mining	Hs.339868	NM_003974	4503358	(RBM8A), mRNA /cds=(12,536) oh47h10.s1 cDNA, 3' end /clone=IMAGE:1469827 /clone_end=3'	1	AGTGACCTTTAGTAGTAATAGTCT TGGCAGCCAGGAACTGAGTATGACA ATGTTGTACTAAAGAAAGGCCCAAA
7248	db mining	Hs.75058	NM_003938	4501976	adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA	1	AGAGAGACATATCACGCTGCTGTC ATGATTTTGTGTCAAGATGATCCA
7247	db mining	Hs.75082	NM_001665	4502218	/cds=(209,3547) ras homolog gene family, member G (rho G) (ARHG), mRNA /cds=(129,704)	1	CTTCTGGGGACCTTTCCTACCCCCAT CAGCATCAATAAAACCTCCTGTCT
7248	db mining	Hs.75309	NM_001961	4503482	eukaryotic translation elongation factor	1	TAGATGATTTCTAGCAGGCAGGAAGT CCTGTGCGGTGTCACCATGAGCAC
7249	db mining	Hs.75725	NM_003564	4507356	2 (EEF2), mRNA /cds=(0,2576) transgelin 2 (TAGLN2), mRNA	1	CCATGGTCTGGGGCTTGAGGAAGAT
7250	db mining	Hs.75770	NM_000321	4506434	/cds=(73,672) retinoblastoma 1 (including osteosarcoma) (RB1), mRNA	1	GAGTTTGTTGATTTAAATAAAGAAT AGGTCAAGGGCTTACTATTTCTGGGT CTTTTGCTACTAAGTTCACATTAG
7251	db mining	Hs.75790	NM_002642	4505794	/cds=(138,2924) phosphatidylinositol glycan, class C	1	TTTCTGGGGACCTCTTGAATTACATG
7252	db mining	Hs.76057	NM_000403	9945333	(PIGC), mRNA /cds=(293,1186) galactose-4-epimerase, UDP- (GALE),	1	CTGTAACATATGAAGTGATGTGGT TGGCACAAAACCTCCTCCTCCCAGGC
7253	db mining	Hs.76662	NM_032327	14150105	mRNA /cds=(76,1122) hypothetical protein MGC2993	1	ACTCATTTATATTGCTCTGAAAGA TGAGGTCACTGCCACTTCTCACATGC
7254	db mining	Hs.77266	NM_002826	13325074	(MGC2993), mRNA /cds=(158,1048) quiescin Q6 (QSCN6), mRNA	1	TGCTTAAGGGAGCACAAATAAAGG CACGCTACCCCCTGCCTTGGGAGGT
7255	db mining	Hs.77290	NM_006755	5803186		1	GTGTGGAATAAATTATTTTTGTTAA AATGCAGAGAATGGAAAGTAGCGCAT
7256	db mining	Hs.77805	NM_001696	4502316		1	CCCTGAGGCTGGACTCCAGATCTG GTGGCACACCACTCCTTCCAGCAGTA
7257	db mining	Hs.78592	NM_001414	4503502	(vacuolar proton pump) 31kD (ATP6E), mRNA /cds=(75,755) eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD) (EIF2B1), mRNA /cds=(10,927)	1	GTCGCTTTACTGTTACCTGTTTAG AGCAACAGTATTCTGCATGGTTCACT GCTTAAGAAAATGCCTTCTGGAAT

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7258	db mining	Hs.78605	BC006159	13544048	Homo sapiens, clone IMAGE:3635549, mRNA, partial cds /cds=(0,891)	1	AAACATGTCCCTGGAGAGTAGCCTGC TCCCACACTGTCACTGGATGTCAT
7259	db mining	Hs.78890	AF171938	5852969	NUMB isoform 1 (NUMB) mRNA, complete cds /cds=(270,2225)	1	CAGTTGCAGCCTCTTGACCTCGGATA ACAATAAGAGAGCTCATCTCAT
7260	db mining	Hs.79150	NM_006430	5453604	complete cus /cus=(2/0,2225) chaperonin containing TCP1, subunit 4 (delta) (CCT4), mRNA /cds=(0,1619)	1	TGGGCTTGGTCTTCCAGTTGGCATTT GCCTGAAGTTGTATTGAAACAATT
7261	db mining	Hs.79259	NM_016404	7705476	hypothetical protein (HSPC152), mRNA /cds=(35,412)	1	TTCTGCCGTGTGTATCCCCAACCCTT GACCCAATGACACCAAACACAGTG
7262	db mining	Hs.79356	NM_006762	5803055	Lysosomal-associated multispanning membrane protein-5 (LAPTM5), mRNA /cds=(75,863)	1	TGTGTGCGACAGGGAGGAAGTTTCA ATAAAGCAACAACAAGCTTCAAGGA
7263	db mining	Hs.79572	NM_001909	4503142	cathepsin D (lysosomal aspartyl protease) (CTSD), mRNA /cds=(2,1240)	1	CTCCCCTTGGGCGGCTGAGAGCCCC AGCTGACATGGAAATACAGTTGTTG
7264	db mining	Hs.81337	NM_009587	6806889	lectin, galactoside-binding, soluble, 9 (galectin 9) (LGALS9), transcript variant long, mRNA /cds=(56,1123)	1	CTCCACCACCTGACCAGAGTGTTCTC TTCAGAGGACTGGCTCCTTTCCCA
7265	db mining	Hs.82030	NM_004184	7710155	tryptophanyl-tRNA synthetase (WARS), mRNA /cds=(187,1602)	1	CTCTGCCCTCCTGTCACCCAGTAGAG TAAATAAACTTCCTTGGCTCCTAA
7266	db mining	Hs.82396	NM_016816	8051620	2',5'-oligoadenylate synthetase 1 (40- 46 kD) (OAS1), transcript variant E18, mRNA /cds=(33,1235)	1	AAATTCCAGCCTTGACTTTCTTCTGT GCACCTGATGGGAGGGTAATGTCT
7267	db mining	Hs.82933	BC008739	14250568	Homo sapiens, protein x 013, clone MGC:3073 IMAGE:3346340, mRNA, complete cds /cds=(101,325)	1	CTGTAGGCCAGGGTGGAATGAAGTC AGCTCCTTTTTATAGTTGAAATACA
7268	db mining	Hs.83753	NM_003091	4507124	small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB), mRNA /cds=(0,695)	1	TTGGCGGGCCATCCCAACAGGTGAT GACCCCACAAGGAAGAGGTACTGTT
7269	db mining	Hs.85838	NM_004207	4759111	solute carrier family 16 (monocarboxylic acid transporters), member 3 (SLC16A3), mRNA /cds=(62,1459)	1	GGAAGATGGAAATAAACCTGCGTGTG GGTGGAGTGTTCTCGTGCCGAATT
7270	db mining	Hs.306565	NM_013341	9558756	clone HQ0688 /cds=UNKNOWN	1	AGTGAGGACAATGTGGCTTGCTCCTT TITGAATCTACAGATAATGCATGT
7271	db mining	Hs.89497	NM_005573	5031876	lamin B1 (LMNB1), mRNA	1	GAGGGTGGGGGAGGGAGGTGGAGG GAGGGAAGGGTTTCTCTATTAAAATG
7272	db mining	Hs.89525	NM_004494		hepatoma-derived growth factor (high- mobility group protein 1-like) (HDGF), mRNA /cds=(315,1037)	1	TGCTGACTGTAGCTTTGGAAGTTTAG CTCTGAGAACCGTAGATGATTTCA
7273	db mining	Hs.92208	NM_003815		a disintegrin and metalloproteinase domain 15 (metargidin) (ADAM15), mRNA /cds=(7,2451)	1	GATTGAGGAAGGTCCGCACAGCCTG TCTCTGCTCAGTTGCAATAAACGTG
7274	db mining		NM_003975	4503632	SH2 domain protein 2A (SH2D2A), mRNA /cds=(86,1255)	1	GATTCTTGTCTGGCTAATAAATCATCA CCAACTGCCTTCTCCTACAGGGA
7275	db mining	Hs.104879	BF347382	11294957	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373)	1	AGATTCTTAGGGCACGTTTGTTCCCC TTGGAGGGTTTTCCACACGGAGTC
7276	db mining	Hs, 105749		3043629	mRNA for KIAA0553 protein, partial cds /cds=(0,3289)	1	GCCATACTCTGGCTGCCTCTTTGCCT TCCTAGGGGCATTTTCTTTAACTT
7277	db mining	Hs.105751	AL138761	8573811	DNA sequence from clone RP11- 16H23 on chromosome 10. Contains the gene KIAA0204 (HSLK) for a protein kinase, the COL17A1 gene for collagen type XVII alpha 1 (BP180), ESTs and GSSs Icds=(0,3557)	1	TGCCTCTTATCTACTTGAGAGCAACA TGTCTTTTCAATCATGGGATTGAC
7278	db mining	Hs.324406	AK026741	10439662	ribosomal protein L41 (RPL41), mRNA /cds=(83,160)	1	TGGACCTGTGACATTCTGGACTATTT CTGTGTTTATTTGTGGCCGAGTGT
7279	db mining	Hs.108371	NM_001950	12669914	E2F transcription factor 4, p107/p130- binding (E2F4), mRNA /cds=(62,1303)	1	TGAAGGTGTCTGTGACCTCTTTGATG TGCCTGTTCTCAACCTCTGACTGA
7280	db mining	Hs.109760	NM_002491	4505360	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12) (NDUFB3), mRNA /cds=(252,548)	1	CCTGGAGTCCCTGAATAAAGATAAGA AGCATCACTGAAGATAATACCTGG
7281	db mining		AF151783	14248494	MEG3 (MEG3) mRNA, complete cds /cds=(52,2253)	1	TTGTCCCGAAGATTTGCGCCTTTAGT GCCTTTTGAGGGGTTCCCATCATC
7282	db mining	Hs.306417	NM_014714	7662193	cDNA FLJ10935 fis, clone OVARC1000661 /cds=(250,936)	1	CTGCTAGGCTCTGCCCACCGGCCAC CAACACTCCTGTAATTCCAATAAAG
7283	db mining	Hs.114199		13672965	602617003F1 cDNA, 5' end /clone=IMAGE:4730856 /clone_end=5'	1	TTAAAATACTGTCATTGGTTGGGAGG GGATTGCATTAAATGATTAGTCCA
7284	db mining	Hs.118786	BF131637	10970677	601820457F1 cDNA, 5' end /ctone=IMAGE:4052246 /ctone_end=5'	1	CTCACACACGCAGGCGACAGTCAGA ACAAACAGGAACAAAGCTACAACAC
7285	db mining		NM_024872	13376307	hypothetical protein FLJ22570 (FLJ22570), mRNA /cds=(0,1490)	1	TGAATAGTGTGCAGACTCACAGATAA TAAAGCTCAGAGCAGCTCCCGGCA
7286	db mining	Hs.123373	AW963279	8153115	602853825F1 cDNA, 5' end /clone=IMAGE:4994982 /clone_end=5'	1	CCCAGTGCTTCACGAAGTTAAAGGAA AGATCTGCTGGTAGTGTTTAGTCT

					Table 6		
7287	db mining	Hs.125078	AF090094	4063629	clone IMAGE 172979 /cds=UNKNOWN	1	CGAGCCGACCATGTCTTCATTTGCTT CCACAAGAACCGCGAGGACAGAGC
7288	db mining	Hs.130740	AK000315	7020316	cDNA FLJ20308 fis, clone HEP07264 /cds=(90,1226)	1	TTTTCCCCCTTTAGTCTCCTGGCTTTT TCCTTTCCCTTCCC
7289	db mining	Hs.132955	AL132665	6137021	mRNA; cDNA DKFZp566E034 (from clone DKFZp566E034); complete cds /cds=UNKNOWN	1	AACCGTTGTGGAAATTATTGGAATT AACTGAGCCAAAGTGATTATGCAT
7290	db mining	Hs.133230	BC000085	12652672	Homo saplens, ribosomal protein S15, clone MGC:2295 IMAGE:3507983, mRNA, complete cds /cds=(14,451)	1	GCCCCGATCCTACACCCTGAGCCT CAGAGCACTGCTACTTTTTAAAATA
7291	db mining	Hs.142677	AK024108	10436406	cDNA FLJ14046 fis, clone HEMBA1006461 /cds=UNKNOWN	1	AAGCGTCTCATGGAGTTCGGACTGGT TGGGGTGATAATATTTGTTTCTTT
7292	db mining	Hs.146170	NM_022842	12383093	hypothetical protein FLJ22969 (FLJ22969), mRNA /cds=(274,2223)	1	AAGCCAGGCTTTGGGATACAAGTTCT TTCCTCTTCATTTGATGCCGTGCA
7293	db mining	Hs.146550	Z82215	3135984	DNA sequence from clone RP1-98O2 on chromosome 22 Contains the 5' end of the APOL2 gene for apolipoprotein L 2, the APOL gene for apolipoprotein L, the MY19 gene for nonmuscle type myosin heavy chain 9. ESTs, STSs and GSSs /cds=(0,5882)	1	AGCTGTCACCACTACAGTAAGCTGGT TTACAGATGTTTTCCACTGAGCAT
7294	db mining	Hs.149846	NM_002213	4504772	Integrin, beta 5 (ITGB5), mRNA /cds=(29,2419)	1	TGAAGGTACATCGTTTGCAAATGTGA GTTTCCTCTCCTGTCCGTGTTTGT
7295	db mining	Hs.151738	NM_004994	4826835	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) (MMP9), mRNA /cds=(19,2142)	1	GGATACAAACTGGTATTCTGTTCTGG AGGAAAGGGAGGAGGTGGAGGTGGG
7296	db mining	Hs.336451	NM_024519	13375657	Nucleoside diphosphate kinase type 6 (inhibitor of p53-induced apoptosis- alpha)	1	CTGCCGCTGCCCAGCCACATCCCTT GGTTTTGTATTTATTTACAGAGTT
7297	db mining	Hs.154276	NM_001186	4502352	BTB and CNC homology 1, basic leucine zipper transcription factor 1 (BACH1), mRNA /cds=(118,2328)	1	TGCAGTAGACGATACAGGTTGCATGT GGACACTCAGTCACATTAACAACT
7298	db mining	Hs.155975,	NM_005608	5032004	protein tyrosine phosphatase, receptor type, C-associated protein (PTPRCAP), mRNA /cds=(63,683)	1	CCCCAACCACAGGCATCAGGCAACC ATTTGAAATAAAACTCCTTCAGCCT
7299	db mining	Hs.159410	NM_014484	7657338	molybdopterin synthase sulfurylase (MOCS3), mRNA /cds=(2,1384)	1	GTACTGAGGTGACTGGTATAGTCTGA TGAGAAAGATGTGGATTGCCATAA
7300	db mining	Hs.160999	AV648418	9869432	AV648418 cDNA, 3' end /clone=GLCBJC04 /clone_end=3'	1	CACTTGTTCAATCATGGAACTTTCTA GAACGCTGCCACTCTTCAAAGGCT
7301	db mining	Hs.164036	NM_002076	4504060	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS), mRNA /cds=(87,1745)	1	TCATCACAGTGTGGTAAGGTTGCAAA TTCAAAACATGTCACCCAAGCTCT
7302	db mining	Hs.164478	NM_022461	11968002	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2 (FLJ21939), mRNA /cds=(379,1557)	1	ACAACCTGATCATTGAAGCCAACTTT GTCCCAGCACATTCCTTAAGTCCT
7303	db mining	Hs.169615	NM_023080	12751496	hypothetical protein FLJ20989 (FLJ20989), mRNA /cds=(52,741)	1	ACTTGATTAGGCTCCGGTTTTCCTTT GGCTTCTGCTTTTCAGTGAATGGC
7304	db mining	Hs,171811	AK023758	10435787	cDNA FLJ13696 fis, clone PLACE2000140 /cds=UNKNOWN	1	TTGCAGACAAATTCCTCTGAGCTTAG CTAGGAGTTCATTATGCTTCCTGT
7305	db mining	Hs.171992	NM_002843	4506314	protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA /cds=(349,4362)	1	ACAGTAGCTTAGCATCAGAGGTTTGC TTCCTCAGTAACATTTCTGTTCTC
7306	db mining	Hs.173373	AB023148	4589505	mRNA for KIAA0931 protein, partial cds /cds=(0,2204)	1	ATGTGAGCCAGAGCATGTTGCAGCAA ATCTATTGTTTGTAAAAATAACAA
7307	db mining	Hs.173638	NM_030756	13540470	transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA /cds=(307,2097)	1	TTTGTGCCATGTGGCTACATTAGTTG ATGTTTATCGAGTTCATTGGTCAA
7308	db mining	Hs.177534	NM_007207	13518225	dual specificity phosphatase 10 (DUSP10), mRNA /cds=(142,1590)	1	AGCCCAACCATTAAAAATTTAATACAA CTTGGTTTCTCCCCCTTTTTCCT
7309	db mining	Hs.177592	NM_001003	4506668	602761378F1 cDNA, 5' end /done=IMAGE:4896906 /done_end=5'	1	GCAAAGAAAGAAGAATCCGAGGAGT CTGATGATGACATGGGCTTTGGTCT
7310	db mining	Hs.179661	BC008791	14250651	Homo sapiens, tubulin, beta 5, clone MGC:4029 IMAGE:3617988, mRNA, complete cds /cds=(1705,3039)	1	TTGAAAAGATGACATCGCCCCAAGAG CCAAAAATAAATGGGAATTGAAAA
7311	db mining	Hs.179986	NM_005803	6552331	flotillin 1 (FLOT1), mRNA /cds=(164,1447)	1	TTTTCCTGACCAAGACTGAGGGATGG GCTGGAGGTTTTCAACTTTGCTAC
7312	db mining	Hs.180859	NM_016139	7705850	16.7Kd protein (LOC51142), mRNA /cds=(81,536)	1	TCTGGGACTGGGCAAATGTTTGTGTG GCCTCCTTAAACTAGCTGTTATGT
7313	db mining	Hs.181301	AK024855	10437263	cDNA: FLJ21202 fis, clone COL00293 /cds=UNKNOWN	1	AACCTAAACGTATTTCACTAACTCTG GCTCCTTCTCCATAAAGCACATTT
7314	db mining	Hs.181311	NM_004539	7262387	asparaginyl-tRNA synthetase (NARS), mRNA /cds=(73,1719)	1	CCACCAAATGCATGTCATGTATTCTC AATAGGCTGTATTCCCAGCAGTCA
7315	db mining	Hs.181391	AL390158	9368848	mRNA; cDNA DKFZp761G2113 (from clone DKFZp761G2113) /cds=(0,564)	1	TGTACAGGTAGCTAACTTTGTAAACG CTGTGTATTCCCTCTGCCCCCATG
7316	db mining	Hs.182281	NM_016407	7705482	hypothetical protein (HSPC164), mRNA /cds=(70,990)	1	TCTCATCATTTCGAAGATAGCAGAGT CATAGTTGGGCACCCAGTGATTGG

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7317	db mining	Hs.183180	NM_016476	13324711	anaphase promoting complex subunit 11 (yeast APC11 homolog) (ANAPC11),	1	CAACAAGGTGGAAACAAGGGCTGGA GCTGCGTTTGTTTTGCCATCACTAT
7318	db mining	Hs.183593	NM_006965	5902161	mRNA /cds=(0,398) zinc finger protein 24 (KOX 17)	1	GAGCATTCCTCAGGGGAGGTCACCT
7319	db mining	Hs.184029	AL137509	6808164	(ZNF24), mRNA /cds=(164,1270) Homo sapiens, clone MGC:2764 IMAGE:2958229, mRNA, complete cds	1	GTGAGGTTCCCAGAACTGTAGTTTT TGCAGGTGTTGACAAGATCCGCCATC TGTAATGTCCTTGGCACAATAAAA
7320	db mining	Hs.187652	AA833892	2907491	/cds=(70,1785) od64g04.s1 cDNA /clone=IMAGE:1372758	1	AAGAGTCTGACTTCTCACTAGGAGCA TGTCTGTTGTACTTACTTCAAACA
7321	db mining	Hs.188751	BG111636	12605142	602282682F1 cDNA, 5' end /clone=IMAGE:4369892 /clone_end=5'	1	CAAACACCAAACCAAGATAACACCGG AACGATAAACAGCAGAAACAGAGA
7322	db mining	Hs.193392	U46120	1184779	expressed unknown mRNA /cds=UNKNOWN	1	TGGGTTTGTCCAGTTCAGGCTAGATG TGCATCATGGCAGGAAGAAGAAG
7323	db mining	Hs.195453	NM_001030	4506710		1	AAGGATGTTCCTTCAGGAGGAAGCA GCACTAAAAGCACTCTGAGTCAAGA
7324	db mining	Hs,196914	D86976	1504025	mRNA for KIAA0223 gene, partial cds /cds=(0,3498)	1	CGGAAGCCACCGTGTGGTTCTTTCAC AGGCACGTTTATTTTGCTGAAATA
7325	db mining	Hs,198281	NM_002654	4505838	pyruvate kinase, muscle (PKM2), mRNA /cds=(109,1704)	1	CCTCCACTCAGCTGTCCTGCAGCAAA CACTCCACCCTCCACCTTCCATTT
7326	dib mining	Hs.200317	AB037825	7243188	mRNA for KIAA1404 protein, partial cds /cds=(64,5841)	1	TCCCTCCTTCCAGTGTTCCTTAGAAC AGACATTTAGGTATCTCAGGTCCT
7327	db mining	Hs.202613	BG284262	13035032	602407238F1 cDNA, 5' end /done=IMAGE;4519449 /clone_end=5'	1	CAGCCGCAGCATCTAAACGAACAACA GAGGAGAACGACGAGGACAGAGTT
7328	dib mining	Hs.210778	AL136679	12052881	mRNA; cDNA DKFZp564C1278 (from clone DKFZp564C1278); complete cds /cds=(104,1690)	1	TCACTGGATTTCTGTGTCTTCACTAG AACACCATTGTCATCTCATATTGA
7329	db mining	Hs.211594	NM_006503	5729990	proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4), mRNA /cds=(12,1268)	1	GCTTCTCTCGCACCCCCAGCACCTCT GTCCCAAAACCTCATTCCCTTTTT
7330	db mining	Hs.226307	NM_004900	4758159	phorbolin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA /cds=(79,651)	1	AGCTGCTCACAGACACCAGCAAAGC AATGTGCTCCTGATCAAGTAGATTT
7331	db mining	Hs.326048	NM_006319	5453905	cDNA FLJ14186 fis, clone NT2RP2005726 /cds=UNKNOWN	1	ATGCTCATGTGGTGTCCCCACCGCC CACTTGTTTGATGTCACTGACTGTC
7332	db mining	Hs.227835	NM_014972	14149656	KIAA1049 protein (KIAA1049), mRNA /cds=(96,2126)	1	GCTGAGTGTGTCGCTCCCTGGTCCA CTGTTTCTCCTATAAATGTAAATGG
7333	db mining	Hs.231967	NM_014423	7656878	ALL1 fused gene from 5q31 (AF5Q31), mRNA /cds=(337,3828)	1	TGCAGCACATTGATAAGATGGTTTCC GTGAGCTATGATAAGATTGAAATT
7334	db mining	Hs.232400	NM_031243	14043071	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230)	1	ATAAATATGCAGTGATATGGCAGAAG ACACCAGAGCAGATGCAGAGAGCC
7335	db mining	Hs.236131	NM_022740	13430859	homeodomain-interacting protein kinase 2 (HIPK2), mRNA /cds=(108,3704)	1	TTGAACCGGGAAGTGGGAGGACGTA GAGCAGAGAAGAGA
7336	db mining	Hs.343556	AF090896	6690188	clone HQ0131 PRO0131 mRNA, partial cds /cds=(0,233)	1	TTTGCTCATTCTAAACTCAAGCTTTTA AGCCTCACAGAATTTACAGGGGT
7337	db mining	Hs.238936	BG538032	13530264	602563534F1 cDNA, 5' end /clone=IMAGE:4688193 /clone_end=5'	1	GCCATAGGCTTACATGGGGCATACTC GTTACACAGTCAGAATGTTTGAAA
7338	db mining	Hs.241412	NM_030882	13562089	apolipoprotein L, 2 (APOL2), mRNA /cds=(477,1490)	1	GGTCTCTCGCTCTGTCTTTCCAGCAT CCACTCTCCCTTGTCCTTCTGGGG
7339	db mining	Hs.241471	AL133642	8599293	mRNA; cDNA DKFZp586G1721 (from clone DKFZp586G1721); partial cds /cds=(0,669)	1	TCAGCACCAAGTCATGTTTAAAAGAC CAGAGAGACAAGCATTTTGCCAAG
7340	dib mining	Hs.245188	NM_000362	9257248	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA /cds=(1183,1818)	1	CGAACCCTGTCTAGAAGGAATGTATT TGTTGCTAAATTTCGTAGCACTGT
7341	db mining	Hs.249170	NM_012476	7110734	ventral anterior homeobox 2 (VAX2), mRNA /cds=(32,904)	1	CAAATGGCCTTGGTCCCGCAGCTTGT GTGCGTGAGTGCAGTGTGAGTGTG
7342	db mining	Hs.258551	NM_012100	6912247	aspartyl aminopeptidase (DNPEP), mRNA /cds=(151,1578)	1	CTCTTGGAAAGACTTCTCTGCCATCC CTTTGCACCTGAGAGGGGAAGTTC
7343	db mining	Hs.259412	BG772376	14083029	602722490F1 cDNA, 5' end /clone=IMAGE:4839143 /clone_end=5'	1	GGCGCGGTGACCCACTTATGGGACT TGGCCTTTCTTTGTTGTTTAA
7344	db mining	Hs.259577	AW665292	7457838	hj02c11.x1 cDNA, 3' end /clone=IMAGE:2980628 /clone_end=3'	1	ACCCAGTTCATGATTACTTCTACTCTT AACACTCAATCCCCCTAATTAAACC
7345	db mining	Hs.259679	AW956608	8146291	EST368678 cDNA	1	TTCGATAAACAGCGTTGACTTGCTTG TACCACTTAAGAGTTGTGAGTGCT
7346	db mining	Hs.265827	NM_022873	13259549	interferon, alpha-inducible protein (clone IFI-6-16) (G1P3), transcript variant 3, mRNA /cds=(107,523)	1	TCCAGAACTTTGTCTATCACTCTCCC CAACAACCTAGATGTGAAAACAGA
7347	db mining	Hs.265891	AK001503	7022798	cDNA FLJ10641 fis, clone NT2RP2005748 /cds=UNKNOWN	1	GGGATCTTTCAAATGGATAGTGAGTT GCCTTTTCCTATAGGTGACAATCA

					Table 8		
7348	db mining	Hs.266456	AW768693	7700715	hk65e11.x1 cDNA, 3' end /clone=IMAGE:3001580 /clone_end=3'	1	AGAGCAAGCATTACAGAAAATAGGTC TGGAAGACAGGAAAAGGACAAAGA
7349	db mining	Hs.267368	NM_017842	8923451	hypothetical protein FLJ20489 (FLJ20489), mRNA /cds=(482,1201)	1	ATGTGTCCTGCCCCTCAGCTCTTTGC CTTATCTGTGTCACTGTCACTTTA
7350	db mining	Hs.267812	NM_003794	4507144	sorting nexin 4 (SNX4), mRNA /cds=(0,1352)	1	TCCTGTGAATTGAATTTCTCTTCAATC AAAGTGCCCCAAACAGAAGCACA
7351	db mining	Hs.272027	NM_012177	6912365	F-box only protein 5 (FBXO5), mRNA /cds=(61,1404)	1	AGGTCCCCTGCCTGGTACAAAGAAAA GCAAAAAGAATTTACGAAGATTGT
7352	db mining	Hs.272534	AL080088	5262475	mRNA; cDNA DKFZp564J062 (from clone DKFZp564J062) /cds≅UNKNOWN	1	GCCAGAAGCATAATTTACCAGAGACG AGAACAGGGTGTGGGAGAGAGAGAA
7353	db mining	Hs.273415	NM_000034	4557304	aldolase A, fructose-bisphosphate (ALDOA), mRNA /cds=(167,1281)	1	TCTTTCTTCCCTCGTGACAGTGGTGT GTGGTGTCGTCTGTGAATGCTAAG
7354	db mining	Hs.273830	AK022804	10434416	cDNA FLJ12742 fis, clone NT2RP2000644 /cds=UNKNOWN	1	CAGTCAAACATTTTACCTTGTGCCTT GGCTCACTCTGTGCCTTTTCTCCA
7355	db mining	Hs.274287	AK001508	7022805	cDNA FLJ10646 fis, clone NT2RP2005773, highly similar to pyrroline 5-carboxylate reductase isoform mRNA /cds=UNKNOWN	1	ACAGGAAACGGGCTTTCTCTGAATTG GTAAATGGGAAAGAAGTGAGCAAC
7356	db mining	Hs.275163	NM_002512	4505408	non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein,	1	GTCCCTGGACACAGCTCTTCATTCCA TTGACTTAGAGGCAACAGGATTGA
7357	db mining	Hs.276818	Al435118	4300940	mRNA /cds=(72,530) th95e09.x1 cDNA, 3' end /clone=IMAGE:2128440 /clone_end=3'	1	ACCCTCGCCACAAGATTCTGCAATCT CCTAAAGTACAGATGAGAAAGGAA
7358	db mining	Hs.278582	AF135794	4574743	AKT3 protein kinase mRNA, complete cds /cds=(0,1439)	1	TGCCAAGGGGTTAATGAAACAAATAG CTGTTGACGTTTGCTCATTTAAGA
7359	db mining	Hs.279535	AK027035	10440049	cDNA: FLJ23382 fis, clone HEP18349 /cds=UNKNOWN	1	CAGTGGCACACCTTAACCAGTCACTA ATTTTCACTGTTGTGAAAGTGATT
7380	db mining	Hs.283007	NM_006227	5453913	phospholipid transfer protein (PLTP), mRNA /cds=(87,1588)	1	CCCAGTGCCACAGAGAAGACGGGAT TTGAAGCTGTACCCAATTTAATTCC
7361	db mining	Hs.283565	NM_005438	4885242	FOS-like antigen-1 (FOSL1), mRNA /cds=(34,849)	1	TGAGCCCTACTCCCTGCAGATGCCAC CCTAGCCAATGTCTCCTCCCCTTC
7362	db mining		AK026646	10439543	cDNA: FLJ22993 fis, clone KAT11914 /cds=UNKNOWN	1	GCAGGGAGGGAGGATAAGTGGGAT CTACCAATTGATTCTGGCAAAACAA
7363	db mining		AF246229		AF246229 cDNA /clone=RB82	1	GGCCACTACCTTTGTTGGAAACAAAG CATAAGGGAGTGAAAGTGTCTAAA
7384	db mining		AF248230	10419515	AF246230 cDNA /clone=RB16	1	GCTGGCCGATCTCTCCCCACAGTT GCAAGAAGCATTTTCAAAGAATAGT
7365	db mining	Hs.285280	AK024885	10437298	cDNA: FLJ21232 fis, clone COL00752 /cds=UNKNOWN	1	ATTGGGATGAAACTACTTTAGCAAAG TCCACAGATCAGAAACCAGACGGT AGGAGACTGGGTGCTATAATTAGATT
7386	db mining	Hs.288038	NM_006625	12056474	TLS-associated serine-arginine protein 1 (TASR1), mRNA /cds=(72,623)	1	ATTTTGAGGCAGACAGAGAGCTGT
7387	db mining	Hs.288283	AK026008		cDNA: FLJ22355 fis, clone HRC08344 /cds=UNKNOWN	1	AGCCTGCAAGGTTAGGACTTGAAGA GGGAAGGTATTTAATAACTGGGCGA
7368	db mining	Hs.289043	AL136719	12052956	mRNA; cDNA DKFZp566G0346 (from clone DKFZp566G0346); complete cds /cds=(278.790)	1	TTAGTGCAGTTGGAATGAATGTGTAT AGGTCAGAGGTCTTCGTGTTCACA
7369	db mining	Hs.289087	AK024468	10440449	mRNA for FLJ00061 protein, partial cds /cds=(0,522)	1	TCACCTCTCAGTTGAAAGATTTCTTCT TTGAAAGGTCAAGACCGTGAACT
7370	db mining	Hs.290494	BF475245	11544422	EST 003 cDNA, 5' end /clone_end=5'	1	AGTCTGGATGTAAGGCCTGCCTCAAA GAGACACTAATGGGAGGGAACAAA
7371	db mining	Hs.290874	BE730505	10144599	601582627F1 cDNA, 5' end /clone=IMAGE:3832302 /clone_end=5'	1	AAAGGAAGAAGCACGATGCAAACAG AAACAAGACGAGACAGAGTGAGCGA
7372	db mining	Hs.332403	NM_024113	13129129	hypothetical protein MGC4707 (MGC4707), mRNA /cds=(72,1067)	1	ACTGCTTCAAGTCTTGACCCCTTTGT GTCTAATAGCTAAACAAACATGTG
7373	db mlning	Hs.292998	AW972292	8162138	EST384381 cDNA	. 1	AACAATAGGAATAAGGTTACTTCAGC CTTAAGGGGCTTATCATACTGCTG
7374	db mining	Hs.293984	NM_032323	14150097	hypothetical protein MGC13102 (MGC13102), mRNA /cds=(161,1345)	1	GACAGGGAAATCTGCCTACCAAGAG GGGTGTGTGTGTCTTTGTGCCCACA
7375	db mining	Hs.295362	AK027365	14041993	cDNA FLJ14459 fis, clone HEMBB1002409 /cds=UNKNOWN	1	AACAAGTCCATGACTCCCAAGGGTTT AAGGACCAATGGTTCAGTGAGACA
7376	db mining	Hs.297964	BF836049	12187621	•	1	ACACTCATACTCATATGTACGTGCTC AGTCGAACGGACTGCAGTCCGTTC
7377	db mining	Hs.299329	AK000770	7021066	/cds=UNKNOWN	1	TACTGCTATGGAATGAGACCACCACT TCTCCTGTTGTCCTTCCCAGCTTC
7378	do mining	Hs.300631	AK022958	10434651	cDNA FLJ12896 fis, clone NT2RP2004194, weakly similar to Rattus norvegicus Golgi SNARE GS15 mRNA /cds=UNKNOWN	1	TGCCAAGTGAGGACAAACTGCTAGG CTGTATCCCATAATTTCAGGATGAG
7379	do mining	Hs.301417	M80899	178282	novel protein AHNAK mRNA; partial sequence /cds=(0,3835)	1	AAACCGACCGCCTGTAGGCTCCTGG AACTATACAGATAGGTAAAGAGTTC
7380	do mining	Hs.301612	NM_005253	4885244	FOS-like antigen 2 (FOSL2), mRNA /cds=(3,983)	1	GACCAATCATCAGACTCCTTGAACTC CCCCACTCTGCTGGCTCTGTAACC
7381	db mining	Hs.301636	NM_000287	4505728	peroxisomal biogenesis factor 6 (PEX6), mRNA /cds=(70,3012)	1	AGAGATCCAGGTGCAAGTGGATTGA GACAGCAGCAACAGCTCAAGAGATA

					Table 8		
7382	db mining	Hs,337774	NM_004723	4758671	rho/rac guanine nucleotide exchange factor (GEF) 2 (ARHGEF2), mRNA	1	ATGTCCCTTTCTCCTCTCCCCTCTTC CTCTTACTGCTGTTCTCCCTTTCT
7383	db mining	Hs.318568	BF475243	11544420	/cds=(112,2988) EST 001 cDNA, 5' end /clone_end=5'	1	ACATCCATAGAACAATACATCAAAGT TGTTGAAGTGTTGCAGGGGAGGGC
7384	db mining	Hs.318569	BF475244	11544421	EST 002 cDNA, 5' end /clone_end=5'	1	AGCACTTACTGTCAGGCATTCAGAAT GTGAGCAATGACAATAATTTACCT
7385	db mining	Hs.321709	NM_002560	4505548	purinergic receptor P2X, ligand-gated ion channel, 4 (P2RX4), mRNA	1	AATCTGATTGAGTCTCCACTCCACAA GCACTCAGGGTTCCCCAGCAGCTC
7386	db mining	Hs.322478	D38491	559327	/cds=(27,1193) mRNA for KIAA0117 gene, partial cds /cds=(0,683)	1	AACCCAAGAAAAGAGTTGCTCTTACT ATCTACTGCTGACTCTTGAACTTT
7387	db mining	Hs.323114	AK023846	10435906	cDNA FLJ13784 fis, clone PLACE4000593 /cds=UNKNOWN	1	TTCGTAGGTGGGCTTTTCCTATCAGA GCTTGGCTCATAACCAAATAAAGT
7388	db mining	Hs.323949	NM_002231	13259537	kangal 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monocional and antibody IA4)) (KAI1), mRNA /cds=(181,984)	1	AGGTGGGCTGGACTTCTACCTGCCC TCAAGGGTGTGTATATTGTATAGGG
7389	db mining	Hs.324507	NM_024524	13375667	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(182,2056)	1	TGTGTCAGAATGGCACTAGTTCAGTT TATGTCCCTTCTGATATAGTAGCT
7390	db mining	Hs.326447	BC004857	13436058	Homo saplens, clone IMAGE:3690478, mRNA, partial cds /cds=(0,71)	1	CTATCAGCCCCAAGTGGAGCAGAAC AGAGGGATTTGGGAGGAATGTCCTC
7391	db mining	Hs.333558	BG577468	13592532	gu.seq cDNA	1	TGCTAAGGAGAGGGGCCATGAAGAG TTTTGTTGAGAACATCGTGTCTGAG
7392	db mining	Hs.334303	BG642392	13777102	gu.seq395250 cDNA	1	AGTCAGAACTTCAAGTCCCCATTAAA GGGGCTGGAAAATACAAGTACAGT
7393	db mining	Hs.334804	NM_000558	6715603	hemoglobin, alpha 1 (HBA1), mRNA	1	CTCCCCTTCCTGCACCCGTACCCCC GTGGTCTTTGAATAAAGTCTGAGTG
7394	db mining	Hs.334853	NM_032241	14149953	/cds=(37,465) hypothetical protein FLJ23544	1	CAGATGGTTGTGGGGTCAAGTACATC
7395	db mining	HS.250655	NM_032695	14249283	(FLJ23544), mRNA /cds=(125,517) Prothymosin, alpha (gene sequence 28)	1	CCCAGTCGTGGCCCTTTGGACAAG TTTTGGCCTGTTTGATGTATGTGTGA
7398	db mining	Hs.336689	AA493477	2223318	ESTs	1	AACAATGTTGTCCAACAATAAACA AGCCTAGGTGACAGAGCAAGACTCC
7397	db mining	Hs.180450	BF791433	12096487	ribosomal protein S24 (RPS24), transcript variant 1, mRNA	1	ATTTCAAAAACAAAACAAAACAAAA ACACTGAGAATACACGACATACACGC ACGCACAAGACAACAACAGACAGC
7398	Table 3A	NA	AA077131	1836605	/cds=(37,429) 7808E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7808E10, mRNA sequence	1	CAGCCACCTCCTCAGGTCAGACAAG CCCAGCACCCAAATACCACTATCTG
7399	Table 3A	NA	AA501725	2236692	ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element;, mRNA	1	GGCTTCCCTATTACCTCCCAGCGAAA TTCGTAGTCTTTCTCTATGGAGTT
7400	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	1	TGCTGATGTGTTAGGTAGTTGTGGCA CACTCACCTGTCTTTCCTAAATGC
7401	Table 3A	NA	AA579400	2357584	nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915561 similar to contains Alu repetitive element;contains	1	TTCATGCTCAGCAAAACAACGTTTTA GGATGGTGAGAGAAAGAAAGTAA
7402	Table 3A	NA	AF249845	8099620	isolate Siddi 10 hypervariable region I, mitochondrial sequence	1	TATTAACCACTCACGGGAGCTCTCCA TGCATTTGGTATTTTCGTCTGGGG
7403	db mining	Hs.277051	Al630242	4681572	ad07c09.y1 cDNA /clone=ad07c09- (random)	1	TTACCTGCTTTGCATGCTCTCCATCG TCAAAGTCTTCTGGAAACTTAGGC
7404	db mining	Hs.277052	Ai630342	4681672	ad08g11.y1 cDNA /clone=ad08g11- (random)	1	CCCCACCCAACACATACAAACGTTT CCCACCAATCCTTGAACTGCAAAA
7405	db mining	NA	AI732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element;, mRNA s	1	TTCAAGGTCCCAATACCCAACTAACT CGAAGGAAGAAATGGAAATCTATT
7406	Table 3A	Hs.197803	AW379049	6883708	mRNA for KIAA0160 gene, partial cds /cds=(0,2413)	1	TGCACAGAACTCTTACTTACATGTCT CATCGAAACTCCAGAACACCGTCG
7407	Table 3A	Hs.232000	AW380881	6885540	/cus-(0,2413) UI-H-Bl0p-abh-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone end=3'	1	TGCATGTATCCCGGTAATTCAAATCC AATTTCACAGCCACTGCTGAATAT
7408	Table 3A	Hs.325568	AW384988	6889647	602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	1	TACAGGAAAATGAAACTAGACGGGTG GGGGACACTAGAATGAAAACCAGT
7409	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	1	AGTITCTGCTTTCAGTGACTGAGGCT TTGCTTTAACCTGGTGACTCCCAA
7410	Table 3A	NA	AW837717	7931691		1	TCCCACTTCAAGTTAAGCACCAAAGC AATCACTAATTCTGGAGCACAGGA
7411	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	1	CATGGATGGGGGCAGTGTTTCT AGTGTGTGAGGAAGCAGAGCAG
7412	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	1	TCACCACAGATGGGAAGATCGTTTCC TGAAAACAGTCTATAAATCACAGA
7413	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	1	CAGACGCTCCAGTGCTGCCGAGGTT AGTGTGTTTATTAGACCTGAAATGA

					Table 8			
7414	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290	1	CCCTTTAGGCCTCTTGCCCGAACAGT	
7415	Table 3A	NA	AW891344	8055549	cDNA, mRNA sequence PM2-NT0079-030500-001-a04 NT0079	1	GAACACTAATAGATATCCTAAGCT ATGGGGATCATGTTTTATTTTTCTCTA	
7416	Table 3A	NA	BE061115	8405765	cDNA, mRNA sequence QV0-BT0041-011199-039-f09 BT0041	1	TATAATGGGCCAGTGTTTCCCA AGCTGTAGACCATAAGCCACCTTCAG	
7417	Table 3A	NA	BE086076	8476469	cDNA, mRNA sequence PM2-BT0672-130400-006-h09 BT0672	1	GTAGTGGTTTGGGAAATCAAGCAA TGTACTTATGCTTGTCTTCTCTACCTG	
7418	Table 3A	NA	BE091932	8482384	cDNA, mRNA sequence IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	1	CCCCAGTCTTGAAGTGGTGGAA GGAGGGTGTGGGAAGCAAGAGAAGA ACATTCTGTTAGGGGCAGAGAAGAA	
7419	Table 3A	Hs.173334	ŖE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	1	GCATCTCCAGCTTTCATAGTTACCCA ACTTGTAAACCAGAAGATGTGCTG	
7420	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	1	GGCCAGTGCCAGACGGTAGCTAGTT GGATGCTAAAGGTAGAATTTAGATA	
7421	Table 3A	Hs.301497	BE168334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	1	GGCATTGTAGGTTGACACCAGCAAAG ACTCAGAGTGACTTGAGCATTGGA	
7422	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	.1	AGCCCATTTGGATATGGCCCATCTTT ACCTAATGGCTACTATAGTGAGGT	
7423	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	1	AATCACAGCAGTAACTCCCAGTAGGA AAGATTCTCAAAGGAATAGTTCTT	
7424	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609	1	AATGGTCAGGCACAGGTAGAATCAAA	
7425	Table 3A	NA	BE247056	9098807	cDNA, mRNA sequence TCBAP1D6404 Pediatric pre-B celi acute lymphoblastic leukemia Baylor-	1	GTCCTGTATGTATGTTCACACAGA TACCTGAAGGTGTAGAGAGTGCCCG CATCCAGCAAGGCCAACAGCTCCAC	
7426	Table 3A	Hs.11050	BE763412	10193336	HGSC project=TCBA cDNA clone T mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	1	CTGTGTTTTTCCCAAAGCAACAATTTC AAACAAAGTGAGAGCCACTGACA	
7427	Table 3A	NA	BF330908	11301656	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	1	GACTCCGAGCTCAAGTCAGTCTGTAC CCCCAACCCCTAACCCACTGCATC	
7428	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	1	TGTAACTGACTTTATGTATCACTCAAG TCTTGCCTTTACTGAGTGCCTGA	
7429	Table 3A	NA	BF364413	11326438	RC6-NN1068-070600-011-B01 NN1068 cDNA, mRNA sequence	1	TCTCTCTAACCAAAACTGTAATCTTCA GGACCAGCAAACTCAGCCCAAGG	
7430	Table 3A	NA	BF373638	11335663	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	1	AACTCTTGGTTAAATGGGTTAATAGA GGATTGGAACACTTTGTTTGCTGT	
7431	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	1	AGAAGCAAACCTGTGAAGCTACTATC GTTTATCATCAGTGTGAATGCACT	
7432	Table 3A	NA	BF749089	12075765	MR2-BN0386-051000-014-b04 BN0386 cDNA, mRNA sequence	1	GGACTAACTTCCACCTCCTCTGCTAC TTCCAGCTGCTTCTAATCACACTT	
7433	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	1	AGTCTTCCACCCAGCATAGGTATCAC ACAACCAGCTCTGTTTTACTCCTG	
7434	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	1	TTAGCTGGTACATTGTTCAGAGTTTA CTGGGAGCCGGTAAGATAGTCACC	
7435	Table 3A	NA.	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	1	AGCGTGATGCTTCCTCATGTCGGTGA TTTTCTGTTGAGACATCTTCAAGC	
7436	Table 3A	NA	BF805164	12134153	QV1-Cl0173-061100-456-f03 Cl0173 cDNA, mRNA sequence	- 1	ACAAAAGTATGGAATTCAATTCTTTTT ATATGCTGCAGCCATGTTCCTGCCCT AGA	
7437	Table 3A	NA	BF818594	12156027	MR3-Cl0184-201200-009-a04 Cl0184 cDNA, mRNA sequence	- 1	TGTAATTGATTTCCGCATAAACGGTC ATTACTGGCACCTATGGCAGCACC	
7438	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	1	GTGATCCACTTGGAGCTGCTACTGGT CCCATTGAGTCCTATAGTACTTCA	
7439	Table 3A	NA.	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	1	TGCCATGAAATCTCTATTAATTCTCAG AAAGATCAAAGGAGGTCCCGTGT	
7440	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	1	CCCACCTGGCAAATCCTCAAGTGTGA CCCTAGTCATCTTTCTCCTTTTGG	
7441	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	1	GCTAAACAGAAAAGAACCTGAAGTAC AGTTCCCGTCTTCAAAGAAGATGC	
7442	Table 3A	N A	BF877979	12268109	MR0-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	1	ATCCTCCTCCCTGGGATGGCATAGA AGAGACTTTAAAACCAAATGAGCC	
7443	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	1	GTCAGTAAGCTCTGCCTGCCAAGAAG ACACAGTGAGAGGTGTCCACAGTC	
7444	Table 3A	NA	BF898285	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	1	GTTTCCACTTAGTTACTTCTTCCTACC TGCTGTGAAGCTCTGCACCCTGC	
7445	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	1	AGAGTAATCCACATCCCAGGGACAGT CACAATGACCTACGGCTTTAGCTG	
7446	Table 3A	Hs.324473	BF904425	12295884	40 kDa protein kinase related to rat ERK2 /cds=(134,1180)	1	GCAGGGCTACACCAAGTCCATTGATA TTTGGTCTGTAGGCTGCATTCTGG	
7447	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	1	TCTTCTCTAAAATGCCCTCCTCTCCTT	
7448	Table 3A	Hs.104679	BF926187	12323197	Homo sapiens, cone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373)	1	TCGCCATTTGGTAGTTCCACAGTGAC TGCTCTTCTATTTTACGAAGCCAC	
7449	Table 3A	Hs.75703	BF928644	12326772	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	1	GTAGATTACTATGAGACCAGCAGCCT CTGCTCCCAGCCAGCTGTGGTGTG	

7450	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03	1	TTTCCTTTTCGCTGACTTTCTCACTCA
7454	Table 3A	NA	F11941	706260	GN0227 cDNA, mRNA sequence HSC33F051 normalized infant brain	1	CTGTCTGTCTCTCATTTTCTCCA TGGTAAGTTTCTGGCAGTGTGGAGAC
7431	Table 3A	NA.	F11941	700200	cDNA cDNA clone c-33f05, mRNA	•	AGGGGAATAATCTCAACAGTAGGT
					sequence		
7452	Table 3A	NA	U46388	1236904	HSU46388 Human pancreatic cancer	1	CCATGGTGGTGCTTGACTTTGCTTTG
					cell line Patu 8988t cDNA clone xs425, mRNA sequence		GGGCTTAATCCTAGTATCATTTGG
7453	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46,	1	TCAGTGGGTGTTGGTTGTCCATTAGT
7400	rabic art		0.0000	1000000	mRNA sequence		TGAGACTTAGTTGTTGCTCTGGGA
7454	Table 3A	NA	W27656	1307658	36f10 Human retina cDNA randomly	1	GGCTGGACAGCAGATGATTCAAATCT
					primed sublibrary cDNA, mRNA		CAATACTACATGCCCATTCTGTGG
7455	literature	NA	X17403	59591	sequence Human cytomegalovirus strain AD169	1	AATAATAGATTAGCAGAAGGAATAAT
/455	illerature	INM	X17403	39351	complete genome	•	CCGTGCGACCGAGCTTGTGCTTCT
7456	literature	NA	X17404	59591	Human cytomegalovirus strain AD169	1	TTTTGCGAACTTTTAGGAACCAGCAA
					complete genome		GTCAACAAAGACTAACAAAGAAA
7457	literature	Hs.2799	X17405	59591	Cartilage linking protein 1	1	GAGATCGACATCGTCATCGACCGAC CTCCGCAGCAACCCCTACCCAATCC
7458	literature	Hs.2159	X17406	59591	mRNA for cartilage specific	1	ACATTCAAAAGTTTGAGCGTCTTCAT
					proteoglycan		GTACGCCGTTTTCGGCCTCACGAG
7459	literature	NA	X17407	59591	Human cytomegalovirus strain AD169	1	CCAACGACACATCCACAAAAATCCCC
	Pt town	No.	V47400	59591	complete genome	1	CATCGACTCTCACAATCGCATCAT CTTTGAGCAGGTTCTCAAGGCTGTAA
7460	literature	NA	X17408	99991	Human cytomegalovirus strain AD169 complete genome	'	CTAACGTGCTGTCGCCCGTCTTTC
7461	literature	NA	X17409	59591	Human cytomegalovirus strain AD169	1	GATGTCCGTCTACGCGCTATCGGCC
					complete genome		ATCATCGGCATCTATCTGCTCTACC
7462	literature	NA	X17410	59591	Human cytomegalovirus strain AD169	1	TCTTCTGGGACGCCAACGACATCTAC CGCATCTTCGCCGAATTGGAAGGC
7463	literature	NA	X17411	59591	complete genome Human cytomegalovirus strain AD169	1	ACGAACAGAAATCTCAAAAGACGCTG
7400	itterature	INC.	X11411	0,000,	complete genome		ACCCGATAAGTACCGTCACGGAGA
7464	literature	NA	X17412	59591	Human cytomegalovirus strain AD169	1	AGAGAACAACAAACCACCACGACGA
					complete genome		TGAAACAAACGCTCAACCAAACA
7465	literature	NA	X17413	59591	Human cytomegalovirus strain AD169	1	CTGCATCGTCGTCGTCCTCCTCT
7400	illeratore	IN/A	X11410	35001	complete genome	•	CGGAGATCGCGACGGAGAAACAAC
7466	literature	NA ·	X17414	59591	Human cytomegalovirus strain AD169	1	CTGAGCCTGGCCATCGAGGCAGCCA
					complete genome		TCCAGGACCTGAGGAACAAGTCTCA
7467	literature	NA	X17415	59591	Human cytomegalovirus strain AD169 complete genome	1	CCTCTGGAGGCAAGAGCACCCACCC TATGGTGACTAGAAGCAAGGCTGAC
7468	literature	NA	X17416	59591	Human cytomegalovirus strain AD169	1	TTCGTGGGCACCAAGTTTCGCAAGAA
					complete genome		CTACACTGTCTGCTGGCCGAGTTT
7469	literature	NA	J01917	209811	Adenovirus type 2, complete genome	1	CTGTGGAATGTATCGAGGACTTGCTT
7470	literature	NA	J01918	209811	Adenovirus type 2, complete genome	1	AACGAGTCTGGGCAACCTTTGGAC GCTGGCCTGCACCCGCGCTGAGTTT
7470	literature	NA.	201910	209011	Adenovirus type 2, complete genome	•	GGCTCTAGCGATGAAGATACAGATT
7471	literature	NA	J01919	209811	Adenovirus type 2, complete genome	1	GGGGCGGTTAGGCTGTCCTCCTTCT
		-					CGACTGACTCCATGATCTTTTTCTG
7472	literature	NA ·	J01920	209811	Adenovirus type 2, complete genome	1	TGTTTGCCTTATTATTATGTGGCTTAT TTGTTGCCTAAAGCGCAGACGCG
7473	literature	Hs.250596	J01921	209811	xy45f10,x1 cDNA, 3' end	1	ACGGTGATCAATATAAGCTATGTGGT
					/clone=IMAGE:2856139 /clone_end=31		GGTGGGGCTATACTACTGAATGAA
7474	literature	NA	J01922	209811	Adenovirus type 2, complete genome	1	TTTCTGCCCTGAAGGCTTCCTCCCCT CCCAATGCGGTTTAAAACATAAAT
7475	literature	N A	J01923	209811	Adenovirus type 2, complete genome	1	GGCTTATGCCCATGTATCTGAACATC
							CAGAGTCACCTTTACCACGTCCTG
7476	literature	NA	J01924	209811	Adenovirus type 2, complete genome	1	CTACTGCCGTACAGCGAAAGCCGCC
7477	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain	-1	CCAACCCGCGAAACGAGGAGATATG CAGATAGTGGTATTTGGGTGCTGGG
, 4,,,	Table on		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1000000	cDNA Library cDNA clone 7B08E10,		CTTGTCTGACCTGAGGAGGTGGCTG
					mRNA sequence		
7478	Table 3A	NA	AA501725	2236692	ng18e12.s1 NCI_CGAP_Lip2 cDNA	-1	AACTCCATAGAGAAAGACTACGAATT TCGCTGGGAGGTAATAGGGAAGCC
					clone IMAGE:929806 similar to contains Alu repetitive element;, mRNA		TCGCTGGGAGGTAATAGGGAAAGCC
					And repeative cieriesis, mitter		
7479	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA	-1	GCATTTAGGAAAGACAGGTGAGTGTG
					clone IMAGE:956346, mRNA sequence		CCACAACTACCTAACACATCAGCA
7480	Table 3A	NA	AA579400	2357584	nf33d05,s1 NCI_CGAP_Pr1 cDNA	-1	TTACTTTGTCTTCTCTCACCATCCTAA
. 100	· upio dri				clone IMAGE:915561 similar to contains	•	AACGTTGTTTTGCTGAGCATGAA
					Alu repetitive element; contains		
7404	Table 24	N/A	AF249845	8000000	isolate Siddi 10 hypervariable region I,	4	CCCCAGACGAAAATACCAAATGCATG
7481	Table 3A	NA	VI.748040	JU0902U	mitochondrial sequence	-1	GAGAGCTCCCGTGAGTGGTTAATA
7482	do mining	Hs.277051	A1630242	4681572		-1	GCCTAAGTTTCCAGAAGACTTTGACG
	•				(random)		ATGGAGAGCATGCAAAGCAGGTAA
7483	db mining	Hs.277052	At630342	4681672	ad08g11.y1 cDNA /clone=ad08g11- (random)	-1	TTTTGCAGTTCAAGGATTGGTGGGAA ACGTTTGTATGTGTTGGGGTGGGG
					(ididoily		ACCITIONATO TO T

					Table 8		
7484	db mining	NA	Al732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element;, mRNA s	-1	AATAGATTTCCATTTCTTCCTTCGAGT TAGTTGGGTATTGGGACCTTGAA
7485	Table 3A	Hs.197803	AW379049	6883708	mRNA for KIAA0160 gene, partial cds /cds=(0,2413)	-1	CGACGGTGTTCTGGAGTTTCGATGAG ACATGTAAGTAAGAGTTCTGTGCA
7486	Table 3A	Hs.232000	AW380881	6885540	UI-H-Bl0p-abh-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035	-1	ATATTCAGCAGTGGCTGTGAAATTGG ATTTGAATTACCGGGATACATGCA
7487	Table 3A	Hs.325568	AW384988	6889647	/clone_end=3' 602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	-1	ACTGGTTTTCATTCTAGTGTCCCCCA CCCGTCTAGTTTCATTTTCCTGTA
7488	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	-1	TTGGGAGTCACCAGGTTAAAGCAAAG CCTCAGTCACTGAAAGCAGAAACT
7489	Table 3A	NA	AW837717	7931691	CM2-LT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	-1	TCCTGTGCTCCAGAATTAGTGATTGC TTTGGTGCTTAACTTGAAGTGGGA
7490	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	-1	CATCTGCTCTGCTTCCTCACACACTA GAAACACCACTGCCCCCATCCATG
7491	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	-1	TCTGTGATTTATAGACTGTTTTCAGGA AACGATCTTCCCATCTGTGGTGA
7492	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	-1	TCATTTCAGGTCTAATAAACACACTAA CCTCGGCAGCACTGGAGCGTCTG
7493	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	-1	AGCTTAGGATATCTATTAGTGTTCACT GTTCGGGCAAGAGGCCTAAAGGG
7494	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	-1	TGGGAACACACTGGCCCATTATATAG AGAAAAATAAAACATGATCCCCAT
7495	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041 cDNA, mRNA sequence	-1	TTGCTTGATTTCCCAAACCACTACCT GAAGGTGGCTTATGGTCTACAGCT
7496	Table 3A	NA	BE086076	8476469	PM2-BT0672-130400-006-h09 BT0672 cDNA, mRNA sequence	-1	TTCCACCACTTCAAGACTGGGGGCA GGTAGAGAAGACAAGCATAAGTACA
7497	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	-1	TTCTTCTCTGCCCCTAACAGAATGTT CTTCTCTTGCTTCCCACACCCTCC
7498	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	-1	CAGCACATCTTCTGGTTTACAAGTTG GGTAACTATGAAAGCTGGAGATGC
7499	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	-1	TATCTAAATTCTACCTTTAGCATCCAA CTAGCTACCGTCTGGCACTGGCC
7500	Table 3A	Hs.301497	BE168334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	-1	TCCAATGCTCAAGTCACCTCTGAGTCT- TTGCTGGTGTCAACCTACAATGCC
7501	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	-1	ACCTCACTATAGTAGCCATTAGGTAA AGATGGGCCATATCCAAATGGGCT
7502	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	-1	AAGAACTATTCCTTTGAGAATCTTTCC TACTGGGAGTTACTGCTGTGATT
7503	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	-1	TCTGTGTGAACATACATACAGGACTT TGATTCTACCTGTGCCTGACCATT
7504	Table 3A	Hs.86543	BE247058	9098807	602495247F1 cDNA, 5' end /clone=IMAGE:4609330 /clone_end=5'	-1	GTGGAGCTGTTGGCCTTGCTGGATG CGGGCACTCTCTACACCTTCAGGTA
7505	Table 3A	Hs.11050	BE763412	10193338	mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	-1	TGTCAGTGGCTCTCACTTTGTTTGAA ATTGTTGCTTTGGGAAAAACACAG
7506	Table 3A	NA	BF330908	11301856	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	-1	GATGCAGTGGGTTAGGGGTTGGGGG TACAGACTGACTTGAGCTCGGAGTC
7507	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	-1	TCAGGCACTCAGTAAAGGCAAGACTT GAGTGATACATAAAGTCAGTTACA
7508	Table 3A	NA	BF364413	11326438	RC6-NN1068-070600-011-B01 NN1068 cDNA, mRNA sequence	-1	CCTTGGGCTGAGTTTGCTGGTCCTGA- AGATTACAGTTTTGGTTAGAGAGA
7509	Table 3A	NA	BF373638	11335663	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	-1	ACAGCAAACAAAGTGTTCCAATCCTC TATTAACCCATTTAACCAAGAGTT
7510	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	-1	AGTGCATTCACACTGATGATAAACGA TAGTAGCTTCACAGGTTTGCTTCT
7511	Table 3A	NA	BF749089	12075765	MR2-BN0386-051000-014-b04 BN0386 cDNA, mRNA sequence	-1	AAGTGTGATTAGAAGCAGCTGGAAGT AGCAGAGGAGGTGGAAGTTAGTCC
7512	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	-1	CAGGAGTAAAACAGAGCTGGTTGTGT GATACCTATGCTGGGTGGAAGACT
7513	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	-1	GGTGACTATCTTACCGGCTCCCAGTA AACTCTGAACAATGTACCAGCTAA
7514	Table 3A	NA	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	-1	GCTTGAAGATGTCTCAACAGAAAATC ACCGACATGAGGAAGCATCACGCT
751 5	Table 3A	NA	BF805164	12134153	QV1-Cl0173-061100-456-f03 Cl0173 cDNA, mRNA sequence	-1	TCTAGGGCAGGAACATGGCTGCAGC ATATAAAAAAGAATTGAATT
7516	Table 3A	NA	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	-1	GGTGCTGCCATAGGTGCCAGTAATG ACCGTTTATGCGGAAATCAATTACA
7517	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	-1	TGAAGTACTATAGGACTCAATGGGAC CAGTAGCAGCTCCAAGTGGATCAC
7518	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	-1	ACACGGGACCTCCTTTGATCTTTCTG AGAATTAATAGAGATTTCATGGCA

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					Table 8		
7519	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119	-1	CCAAAAGGAGAAAGATGACTAGGGT
7520	Table 3A	NA	BF875575	12265705	cDNA, mRNA sequence QV3-ET0100-111100-391-c02 ET0100	-1	CACACTTGAGGATTTGCCAGGTGGG GCATCTTCTTTGAAGACGGGAACTGT
7521	Table 3A	NA	BF877979	12268109	cDNA, mRNA sequence MR0-ET0109-171100-001-b02 ET0109	-1	ACTTCAGGTTCTTTTCTGTTTAGC GGCTCATTTGGTTTTAAAGTCTCTTCT
7522	Table 3A	NA	BF897042	12288501	cDNA, mRNA sequence IL2-MT0179-271100-254-C11 MT0179	-1	ATGCCATCCCAGGGGAGGAGGAT GACTGTGGACACCTCTCACTGTGTCT
7523	Table 3A	NA	BF898285	12289744	cDNA, mRNA sequence QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	-1	TCTTGGCAGGCAGAGCTTACTGAC GCAGGGTGCAGAGCTTCACAGCAGG TAGGAAGAAGTAACTAAGTGGAAAC
7524	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211	-1	CAGCTAAAGCCGTAGGTCATTGTGAC
7525	Table 3A	Hs.324473	BF904425	12295884	cDNA, mRNA sequence 40 kDa protein kinase related to rat ERK2 /cds=(134,1180)	-1	TGTCCCTGGGATGTGGATTACTCT CCAGAATGCAGCCTACAGACCAAATA TCAATGGACTTGGTGTAGCCCTGC
7526	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	-1	TTTAAACCAGGTCTGGAAAAAGGAAG GAGAGGAGGGCATTTTAGAGAAGA
7527	Table 3A	Hs.104679	BF926187	12323197	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373)	-1	GTGGCTTCGTAAAATAGAAGAGCAGT CACTGTGGAACTACCAAATGGCGA
7528	Table 3A	Hs.75703	BF928644	12326772	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	-1	CACACCACAGCTGGCTGGGAGCAGA GGCTGCTGGTCTCATAGTAATCTAC
7529	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	-1	TGGAGAAAATGAGAGACAGACAGTG AGTGAGAAAGTCAGCGAAAAGGAAA
7530	Table 3A	NA	F11941	706260	HSC33F051 normalized Infant brain cDNA cDNA clone c-33f05, mRNA sequence	-1	ACCTACTGTTGAGATTATTCCCCTGT CTCCACACTGCCAGAAACTTACCA
7531	Table 3A	NA ·	U46388	1236904	HSU46388 Human pancreatic cancer cell line Patu 8988t cDNA clone xs425, mRNA sequence	-1	CCAAATGATACTAGGATTAAGCCCCA AAGCAAAGTCAAGCACCACCATGG
7532	Table 3A	NA ·	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	-1	TCCCAGAGCAACAACTAAGTCTCAAC TAATGGACAACCAACACCCACTGA
7533	Table 3A	NA	W27656	1307658	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	-1	CCACAGAATGGGCATGTAGTATTGAG ATTTGAATCATCTGCTGTCCAGCC
7534	literature	Hs.99982	BC005929	13543541	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein) (PRG2), mRNA /cds=(857,1525)	1	TACTGGCGTCGAGCCCACTGCCTCA GAAGACTTCCTTTCATCTGTTCCTA
7535	literature	Hs.48295	X14346	31182	eosinophil peroxidase (EPX), mRNA /cds=(0,2147)	1	GTTTCAAGGGACATCTTCAGAGCCAA CATCTACCCTCGGGGCTTTGTGAA
7538	literature	Hs.1258	J05225	179076	arylsulfatase B (ARSB), mRNA /cds=(559,2160)	1	CTACAGTTCTACCATAAACACTCAGT CCCCGTGTACTTCCCTGCACAGGA
7537	literature	Hs.728	M28129	556208	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA /cds=(71,556)	1	TAGTTGCATGTGACAACAGAGATCAA CGACGAGACCCTCCACAGTATCCG
7538	Ilterature	Hs.889	NM_001828	6325464	Charot-Leyden crystal protein (CLC), mRNA /cds=(33,461)	1	TTGACCATAGAATCAAGCCTGAGGCT GTGAAGATGGTGCAAGTGTGGAGA
7539	literature	Hs.135828	M69138	180539	chymase 1, mast cell (CMA1), mRNA /cds=(0,743)	1	CTGCTGTCTTCACCCGAATCTCCCAT TACCGGCCCTGGATCAACCAGATC
7540	literature	Hs.334455	NM_003293	13699841	tryptase, alpha (TPS1), mRNA /cds=(17,844)	1	GTCACTGGAGGACCAACCCCTGCTG TCCAAAACACCACTGCTTCCTACCC
7541	literature	NA -	NC_001345	9625578	Human herpesvirus 4, complete genome	1	CATGCCATGCATATTTCAACTGGGCT GTCTATTTTTGACACCAGCTTATT
7542	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	GAGAAGCACCTCAACCTGGAGACAAT TCTACTGTTCAAACAGCAGCAGCA
7543	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	ACTTGTCAGGGCCATTCTCTCCGG GCACTGGGTCACTAGGACTGTTTT
7544	literature	NA NA	NC_001345	9625578 9625578	Human herpesvirus 4, complete genome	1	GACAGCGTCCTAGAAACCCTGGCGA, CCATTGCCTCCAGCGGGATAGAGTG
7545 7546	literature literature	NA .	NC_001345 NC_001345	9625578	Human herpesvirus 4, complete genome Human herpesvirus 4, complete	1	CATCCTCTGGAGCCTGACCTGTGATC GTCGCATCATAGACCGCCAGTAGA GCCTCCACACGACATCACACCATATA
7547	literature	Hs.279852	BC004555	13528716	genome G protein-coupled receptor (G2A),	1	CCGCAAGGAATATCAGGGATGCTG ACAGCCATCCTCCCCTTGAGAGTCAT
7548	literature	NA NA	NC 001345	9625578	mRNA /cds=(900,2042) Human herpesvirus 4, complete	1	CAGAAAAATACATTAGGAAAATGT ACCTTCGTCTTCTGAGTCTCATGCCT
7549	literature	NA NA	NC_001345	9625578	genome Human herpesvirus 4, complete	1	CAAAACCTAGTTTGATAGACAGGA AGATGGCTACCCTTCTGATTATGATC
7550	literature	NA.	NC_001345	9625578	genome Human herpesvirus 4, complete	1	CTTTCGTAGAAAATGCTCAAATCT ATGCATCGCCGACAAGTCTTGAATTA
7551	literature	NA.	NC_001345	9625578	genome Human herpesvirus 4, complete	1	GGATTGTCGAAATTAGACAAAGAA CGGGTGTGTTCAATCATCGACGGTGA
7552	literature	NA	NC_001345	9625578	genome Human herpesvirus 4, complete	1	CAATCCTATCTCCATCTATAATCC GAAGAGCGAAATGCAATCTTCTGCTT
7553	literature	NA	NC_001345	9625578	genome Human herpesvirus 4, complete	1	CTTCAGTAGAGACTTTACAGTCTT GCACATCCATCGCCCAAAGTGAAGTC
7554	literature	NA	NC_001345	9625578	genome Human herpesvirus 4, complete genome	1	TGCAAGGATGCCATTTATTGGTTG TCTCGGTTTACCTTTTTGCTGTTGTG GTTCTTTGTTCTTGCTGGTTTGCT

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7555	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	TCTGAATACTCTACAAAACGCTCCTT GTCTGCTCTTAAAACCATCTGTGT
7556	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	TGAAGCTGACACCTGTGAAACTAACT TAAACGCATGTTCTTCTGACTCAG
7 5 57	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	TTCTGTTTTGGGCCAGGAACCGTTCT ATAAATTGTTTTATTGACTACACG
7558	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	TAACACCGTCCAAGAAATTTTGCCGT TGTGTCCCCATACTTCTCTAGGGC
7559	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	AGAAGAAGGATCAGATGGAGAGTTG AAAACTTTAGCTGGTAAGTACATGA
7560	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	CCGATACCGGCAAGATCTGTCGTCTG GCAAACTCGTTTTCCACCTTATGG
7561	literature	NA	NC_001664	9628290	Human herpesvirus 6, complete genome	1	CTGTGGGTCCCTCCCCCTCATCTGTT ATTCCCTTCCCCTCTGCCACCGAT
7562	db mining	Hs.159568	Al382620	4195401	qz04e10.x1 cDNA, 3' end /clone=IMAGE:2020554 /clone_end=3'	1	ACTACATTITAATTAAAGATTAATGGG CATATTAGAAGTTTCTCAAAGTTAGG CT
7563	db mining	Hs.129055	NM_002540	4505490	Homo sapiens, Similar to outer dense fiber of sperm tails 2, clone MGC:9034 IMAGE:3874501, mRNA, complete cds /cds=(656,2947)	1	AAAAGGAGTGAGCTATCATCAGTGCT GTGAAATAAAAGTCTGGTGTGCCA
7564	db mining	Hs.12329	AB014597	3327207	mRNA for KIAA0697 protein, partial cds /cds=(0,2906)	1	AAAGCCACCACTGTTCCCAGTCAGCA TATACAAGCTCTTAATATTCTGTT
7565	do mining	Hs.119177	NM_001659	4502202	ADP-nibosylation factor 3 (ARF3), mRNA /cds=(311,856)	1	AAATGTGGGATAACGCGATGACTGTG ACCCTGGTTGGAAATTAAACTTGT
7568	db mining	Hs.12379	BC003376	13097227	Homo sapiens, ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R), clone MGC:5084 IMAGE:2901220, mRNA, complete cds /cds=(142,1122)	1	AACACAGAAACATTTGAGCATTGTAT TTCTCGCATCCCTTCTCGTGAGCG
7567	db mining	Hs.319886	AL589290	13243062	DKFZp451F1715_r1 cDNA, 5' end /clone=DKFZp451F1715 /clone_end=5'	1	AACCTATCAAAGCCTAGCCTAAGGGC TGCCATCTCTGTCTAAATTCTAGT
7568	db mining	Hs.315597	NM_015960	7705727	cDNA FLJ10280 fis, clone HEMBB1001288, highly similar to CGI- 32 protein mRNA /cds=UNKNOWN	1	AACTGCATGGTATGAATTCAGAGTGT GACTTAAGGGTCAATTCAAAGCAG
7569	db mining	Hs.110457	AF071594	3249714	MMSET type I (WHSC1) mRNA, complete cds /cds=(29,1972)	1	ACAGACTTTGTTAATGTAGGAAATCT CTCCAAGTGGAAACGTGCTAACTT
7570	db mining	Hs.144904	NM_006311	5454137	nuclear receptor co-repressor 1 (NCOR1), mRNA /cds=(240,7562)	. 1	ACAGGCAATTCAGTGGACTATAATAA TAGTGGAGGGTTGAGATGTAGAGT
7571	db mining	Hs.118064	NM_022731	12232386	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA	1	ACAGGTCACAGTGGATTTCTTTTCAA ACTGACAATGTTTAGGTTTTAAGC
7572	db mining	Hs.337616	NM_000753	4502924	/cds=(66,557) phosphodiesterase 3B, cGMP-inhibited (PDE3B), mRNA /cds=(0,3338)	1	ACCTCAAGCAGATGAGATTCAGGTAA TTGAAGAGGCAGATGAAGAGGAAT
7573	db mining	Hs.152049	AW982287	8152099	EST374360 cDNA	1	ACCTT CTACACCACTGGAAAATAACA TGGAGGTTTAGAGCCGTGCAAAAT
7574	db mining	Hs.115325	NM_003929	4506374	RAB7, member RAS oncogene family- like 1 (RAB7L1), mRNA /cds=(40,651)	1	ACTAAACTCTGAGGCCTGAAGTTCTG TGATAGACCTTAAATAAGTGTCCT
7575	db mining	Hs.119178	AK024466	10440445	mRNA for FLJ00059 protein, partial cds /cds=(2624,4057)	1	ACTGGGGTGGTGATGTTTTCGTTCTG TTTTATTTTTCTAACTCTGCTGAC
7576	db mining	Hs.183698	NM_000269	4557796	ribosomal protein L29 (RPL29), mRNA /cds=(29.508)	1	ACTTCATCATAATTTGGAGGGAAGCT CTTGGAGCTGTGAGTTCTCCCTGT
7577	db mining	Hs.15767	AB023166	4589541	mRNA for KIAA0949 protein, partial cds /cds=(0,2822)	1	AGAACGAGGAAGAACACAAGGAA TGATTCAAGATCCACCTTGAGAGGA
7578	db mining	Hs.108104	NM_003347	4507788	ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA /cds=(15,479)	1	AGAGAATAGGCTTTCTAAGATGCTGC GATCCCGTTCTGCTGCCCGTAATA
7579	db mining	Hs.163593	NM_000980	11415025	ribosomal protein L18a (RPL18A), mRNA /cds=(19,549)	1	AGCACAAGCCACGCTTCACCACCAA GAGGCCCAACACCTTCTTCTAGGTG
7580	db mining	Hs.121044	L39061	632997	transcription factor SL1 mRNA, partial cds /cds=(0,1670)	1	AGGCCAATCACTGCTGACTAAGAATT CATTATATTGGCTTAGTACACAGA
7581	db mining	Hs,309348	NM_032472	14277125	tc93c11.x1 cDNA, 3' end /clone=IMAGE:2073716 /clone_end=3'	1	AGGGAAGATTTCTGTATACTTGCTGG AGAGGAGGAATGTGTATAGTTACT
7582	db mining	Hs.16493	AK027866	14042851	cDNA FLJ14960 fis, clone PLACE4000192, weakly similar to ZINC FINGER PROTEIN 142 /cds=(114,3659)	1	AGTTTTAATACCTTAAGCTTTTTCAAG ACCTAACTGCAGCCGCTTTGGGA
7583	db mining	Hs.1342	NM_001862	4502982	cytochrome c oxidase subunit Vb (COX5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(21,410)	1	ATGTGCTGTAAAGTTTCTTCTTTCCAG TAAAGACTAGCCATTGCATTG
7584	db mining		NM_005918	5174540	malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(86,1102)	1	ATTGTGGGTGGCTCTGTGGGCGCAT CAATAAAAGCCGTCCTTGATTTTAT
7585	dib mining	Hs.107476	NM_006476	5453560	ATP synthase, H+ transporting, mitochondrial F1F0, subunit g (ATP5JG), mRNA /cds=(73,384)	1	ATTTGAGTGTTGTTGGACCATGTGTG ATCAGACTGCTATCTGAATAAAAT

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7586	db mining	Hs.146354	NM_005809	5902725	peroxiredoxin 2 (PRDX2), mRNA	1	CAAGCCCACCCAGCCGCACACAGGC CTAGAGGTAACCAATAAAGTATTAG
7587	db mining	Hs.12124	NM_018127	11875212	/cds=(89,685) elaC (E. coli) homolog 2 (ELAC2), mRNA /cds=(0,2480)	1	CACCAGAGACAAGCAGAGTAACAGG ATCAGTGGGTCTAAGTGTCCGAGAC
7588	db mining	Hs.154023	AB011145	3043669	mRNA for KIAA0573 protein, partial cds /cds=(0,1356)	1	CAGGAGGTAGGGATCTGGCTGAGAG GGAATAATCTGAGCAAAGGTATGAA
7589	db mining	Hs.109051	NM_031286	13775197	SH3BGRL3-like protein (SH3BGRL3), mRNA /cds=(71,352)	1	CAGTCCCTCTCCCAGGAGGACCCTA GAGGCAATTAAATGATGTCCTGTTC
7590	db mining	Hs.125307	AA836204	2910523	od22g11.s1 cDNA /clone=IMAGE:1368740	1	CATGAGAAGTATCTGCAATAACCCCA AGTCAACATTTAGGTTTGTGTACA
7591	db mining	Hs.16803	NM_018032	8922296	LUC7 (S. cerevisiae)-like (LUC7L), mRNA /cds=(71,1048)	1	CATGTTGAGTAGGAATAAATAAATCT GATGCTGCCTCCTGAGGCTGCGGG
7592	db mining	Hs.146580	NM_001975	5803010	enolase 2, (gamma, neuronal) (ENO2), mRNA /cds=(222,1526)	1	CCACCACCTCTGTGGCATTGAAATGA GCACCTCCATTAAAGTCTGAATCA
7593	db mining	Hs.14169	AK027567	14042333	cDNA FLJ14661 fis, clone NT2RP2002710, weakly similar to SH3- BINDING PROTEIN 3BP-1	1	COATGCCGCCTCGTTGGATTGTCGG AATGTAGACAGAAATGTACTGTTCT
7594	db mining	Hs.118625	NM_000188	4504390	/cds=(70,2481) hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, mRNA	1	CCCACCGCTTTGTGAGCCGTGTCGTA TGACCTAGTAAACTTTGTACCAAT
7595	db mining	Hs.144505	NM_015653	13124762	/cds=(81,2834) DKFZP566F0546 protein (DKFZP566F0546), mRNA /cds=(377,1306)	1	CCCACGGGAGACTATTTCACACAATT TAATACAGGAAGTCGATAATGAGG
7596	db mining	Hs.155751	NM_004889	4757811	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 (ATP5J2), mRNA /cds=(27,311)	1	CCCTCCGTGAGGAACACAATCTCAAT CGTTGCTGAATCCTTTCATATCCT
7597	db mining	Hs.10267	NM_015367	7662505	MIL1 protein (MIL1), nuclear gene encoding mitochondrial protein, mRNA /cds=(71,1231)	1	CCGTGTCTTTCCAGCCCTAAAGGAAG GGCAGACCCGTGTCTTTCCATGCC
7598	db mining	Hs.14632	BC008013	14124973	Homo sapiens, Similar to CG12113 gene product, clone IMAGE:3532726, mRNA, partial cds /cds=(0,2372)	1	CCTGAAGCACTTCACCTGGAATTGAT GTGTAGGCTTAAGGAGTATGTGAC
7599	db mining	Hs.125156	NM_001488	4503956	transcriptional adaptor 2 (ADA2, yeast, homolog)-like (TADA2L), mRNA /cds=(0,1091)	1	CGCAGGCAAGAGCACTCATCAAGATA GATGTGAACAAAACCCGGAAAATC
7600	db mining	Hs.159545	NM_013308	7019400		1	CGCTCAAAGGTCACTGAGACTTTTGC CTCACCTAAAGAGACCAAGGCTCA
7601	db mining	Hs.152936	NM_004068	4757993	adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA /cds=(135,1442)	1	CGGCCTCAGTCCCTACTCTGCTTTGG GATAGTGTGAGCTTCATTTTGTAC
7602	db mining	Hs.110857	NM_016310	7706498	polymerase (RNA) III (DNA directed) polypeptide K (12.3 kDa) (POLR3K), mRNA /cds=(39,365)	1	CTAGTGTGTGCTTGCCTTGTCCCTCG GGGTAGATGCTTAGCTGGCAGTAT
7603	db mining	Hs.118666	NM_025207	13376805	hypothetical protein PP591 (PP591), mRNA /cds=(820,1704)	1	CTTTCAGATTCCCTCTGGTCTCCGTC CGAAACGTCTACCTCTTCCCAGGC
7604	db mining	Hs.16390	AK024453	10440419	mRNA for FLJ00045 protein, partial cds /cds=(106,924)	1	GAAATTCACAGGCCAGGGCACATCTT TTATTTATTTCATTATGTTGGCCA
7605	db mining	Hs.109302	AA808018	2877424	nv64d09.s1 cDNA, 3' end /clone=IMAGE:1234577 /clone_end=3'	1	GACTCCCTCAACACCCCAAAACTCTA AATGCCACGGTCATCTGTTTCTAT
7606	db mining	Hs.111126	NM_004339	11038670	pituitary tumor-transforming 1 interacting protein (PTTG1IP), mRNA /cds=(210,752)	1	GAGCAGCCACAAAACTGTAACCTCAA GGAAACCATAAAGCTTGGAGTGCC
7607	db mining	Hs.127376	NM_021645	11063982	KIAA0266 gene product (KIAA0266), mRNA /cds=(733,3033)	1	GCAGCAAACAGAGGGTCAGTCACAG GATGTTCTGACACACCATTGTAACT
7608	db mining	Hs.108196	NM_016095	7706366	HSPC037 protein (LOC51659), mRNA /cds=(78,635)	1	GCCAACAATGCTGACCGGTGCTTATC CTCTAAGCCCTGATCCACAATAAA
7609	db mining	Hs.117487	AF040965	2792365	unknown protein IT12 mRNA, partial cds /cds=(0,2622)	1	GCCAGTGTAATTTCTGTCAACCACGG ACGTTTGCCTTCATGTGTAGAATT
7610	db mining	Hs.107882	NM_018171	8922576	hypothetical protein FLJ10659 (FLJ10659), mRNA /cds=(38,1000)	1	GCCCAAGCACTAGTAGAGATGCGCG ATACAGGTCTAGTTTCGGTAACTGT
7611	db mining	Hs.147585	NM_024785	13376147	hypothetical protein FLJ22746 (FLJ22746), mRNA /cds=(266,1072)	1	GGCCAGATTTTGACTCCCAGATTCCT TTACAAAACGCACTCATTCATTCA
7612	db mining	Hs.153357	NM_001084	4505890	procollagen-lysine, 2-oxoglutarate 5- dioxygenase 3 (PLOD3), mRNA /cds=(216,2432)	1	GGGACTCCCCGCGTGATAAATTATTA ATGTTCCGCAGTCTCACTCTGAAT
7613	db mining	Hs.148495	NM_002810	5292160		1	GGGACTGCATGGGAAGCACGGAATA TAGGGTTAGATGTGTGTTATCTGTA
7614	db mining	Hs.13144	NM_014182	7661819	HSPC160 protein (HSPC160), mRNA /cds=(53,514)	1	GGGGTTCGTGTCTTTGGCATCAACAA ATACTGAGGGATGGGTTTTGGGAC
7615	db mining	Hs.1189	NM_001949	12669913	E2F transcription factor 3 (E2F3) mRNA, complete cds /cds=(66,1463)	1	GGGTGACCTGTTCTCTAGCTGTGATC TTACCACTTCAAATGGGTGTAATT
7616	db mining	Hs.12284	BC001699	12804564	Homo sapiens, clone IMAGE:2989556, mRNA, partial cds /cds=(0,370)	1	GGTGTGAACGGGCTGACTTGGTGAA TTGGGCAACTCCTTATAGTGTTGTG

					Table 8		
7617	db mining	Hs.158380	Al381581	4194362	td05e04.x1 cDNA, 3' end /clone=IMAGE:2074782 /clone_end=3'	1	GTACCACTTGAATGATTTCAGTCAATT TTGAACCCCTTTGGAAAGAGGTG
7618	db mining	Hs.1390	BC000268	12653014	Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 2, clone MGC:1664 IMAGE:3352313, mRNA, complete cds /cds=(58,663)	1	GTGAAACCCCGTCTCTGCTAAAAATA CAAAAATTAGCTGGGCGTGGTGGC
7619	db mining	Hs.115808	NM_002287	11231175	leukocyte-associated Ig-like receptor 1 (LAIR1), transcript variant a, mRNA /cds=(57,920)	1	GTTCTCTGGGTTGTGCTTTACTCCAC GCATCAATAAATAATTTTGAAGGC
7620	db mining	Hs.119960	AL117477	5911950	/cus=(07,920) mRNA; cDNA DKFZp727G051 (from clone DKFZp727G051); partial cds /cds=(0,1423)	1	TACTGCCAACTGACCTTATAACCCTC TGCACCTTCAAAAAGATTCATGGT
7621	db mining	Hs.154073	NM_005827	5032212	UDP-galactose transporter related (UGTREL1), mRNA /cds=(87,1055)	1	TCAAACAGTGACATCTCTTGGGAAAA
7622	db mining	Hs.11747	NM_017798	8923363	hypothetical protein FLJ20391	1	TGGACTTAATAGGAATATGGGACT TCACTTCCTCTGAACTGTTACTGCCT
7623	db mining	Hs.10881	AB011113	3043605	(FLJ20391), mRNA /cds=(9,602) mRNA for KIAA0541 protein, partial cds /cds=(0,3484)	1	GAATGGAGTCCTGGACGACATTGG TCCACTTAATAGACTCTATGTGTGCT GAATGTTCCTGTGTACATATGTGT
7624	db mining	Hs.153850	AK024476	10440465	mRNA for FLJ00069 protein, partial cds /cds=(2657,4396)	1	TCCCGCAGAGTGCAGAGACAGGAAG CTGGAGATGTCTTTATAAAGTCACA
7625	db míning	Hs.247870	AL035694	4678462	DNA sequence from clone 33L1 on chromosome 6q14.1-15. Contains the gene for novel T-box (Erachyury) family protein. Contains ESTs, STSs, GSSs and two putative CpG islands /cds=(0.1505)	1	TCTAGGACCCTAGGAAGCTTAACTCT GTCATCATCTCAAGTATCTGCACA
7626	db mining	Hs.324648	NM_003128	4507194	cDNA FLJ13700 fis, clone PLACE2000216, highly similar to SPECTRIN BETA CHAIN, BRAIN /cds=UNKNOWN	1	TCTTCCGCCATCTCCTCTGATAAACA CGAGGTGTCTGCCAGCACCCAGAG
7627	db mining	Hs.118722	NM_004480	4758407	fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA /cds=(716,2443)	1	TGATATGTTGATCAGCCTTATGTGGA AGAACTGTGATAAAAAGAGGAGCT
7628	do mining	NA	AL134726	6602913	DKFZp547A1290_r1 cDNA, 5' end /clone=DKFZp547A1290 /clone_end=5'	1	TGCAGTATTTTTCAAACTTCTGGTCG CAAACCCATTAGTAGTTTGTGAAA
7629	db mining	Hs.166887	NM_003915	4503012	copine I (CPNE1), mRNA /cds=(156,1769)	1	TGCTGCTCTTGATCCCACCTTTGCTC CTGACAACCCTCATTCAATAAAGA
7630	db mining	Hs.146324	AK023182	10434993	cDNA FLJ13120 fis, clone NT2RP3002682, highly similar to CGI- 145 protein mRNA /cds=(176,961)	1	TGGTTTGTTCATGGATGTATTCTAAG AGCTGAGAACAGGGCCTGGACACA
7631	db mining	Hs.12436	AK026309	10439130	cDNA: FLJ22656 fis, clone HSI07655 /cds=UNKNOWN	1	TGTTCTGAATGTTGGTAGACCCTTCA TAGCTTTGTTACAATGAAACCTTG
7632	db mining .	Hs.15164	NM_006333	5453582	nuclear DNA-binding protein (C1D), mRNA /cds=(117,542)	1	TGTTGATGGATGAATTTTGGCATGAT GACTGTACTCTCAATAAAGGCTGA
7633	db mining	Hs.130743	AA642459	2567677	ns30d01.s1 cDNA, 3' end /clone=IMAGE:1185121 /clone_end=3'	1	TTCATCCTGTGAGTGCTGGGGAGGA GGAGTAGATACAGACTGAGTGAGAG
7634	db mining	Hs.16492	NM_015497	13794264	DKFZP564G2022 protein (DKFZP564G2022), mRNA /cds=(42,1709)	1	TTCATTTTCCTGGGAAGTCAAGGTTA CATCTTGCAGAGGTTGTTTTGAGA
7635	db mining	Hs.122552	NM_016426	7705291	G-2 and S-phase expressed 1 (GTSE1), mRNA /cds=(70,2232)	1	TTCTAAGCCGAACCAAATCCTTTGCC TTGAAAGAACAGCCCTAAAGTGGT
7636	db mining	Hs.312510	Al174807	6361196	HA2528 cDNA	1	TTTGTTTGTTTGTTTCAGATAGGGTCT CCCTCTGTCACCCAGGCTGCAGT
7637	db mining	Hs.108258	NM_012090	10048480	actin cross-linking factor (ACF7), transcript variant 1, mRNA /cds=(51,16343)	1	TTTTGTAAATCACGGACACCTCAATTA GCAAGAACTGAGGGGAGGG
7638	db mining	Hs.111092	NM_024724	13376033	hypothetical protein FLJ22332 (FLJ22332), mRNA /cds=(275,1255)	1	CGGTGTGGAAAATGTTGTCCTTTGAG TGGCAAGAATTAGAAAAATCTTCA
7639	db mining	Hs.114311	NM_003504	4502712	CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like (CDC45L), mRNA /cds=(24,1724)	1	CTGAAAGCTGAGGATCGGAGCAAGT TTCTGGACGCACTTATTTCCCTCCT
7640	db mining	Hs.11081	NM_025241	13376853	UBX domain-containing gene 1 (UBXD1), mRNA /cds=(96,1421)	1	GTTGGCCTCAGCCCTGTGGGTCTGT CTCATGCTCTCCCTGTTCCTCTCCC
7641	db mining	Hs.100217	NM_005892	5174400	formin-like (FMNL), mRNA /cds=(39,1430)	1	TAGCCATACTTAGCCTCAGCAGGAGC CTGGCCTGTAACTTATAAAGTGCA
7642	db mining	Hs.12258	AL137728	6808258	mRNA; cDNA DKFZp434B0920 (from clone DKFZp434B0920) /cds=UNKNOWN	1	TGAGGGCTGTGCTGACCTTTGAGAG GATTTGAAATTGCTTCATATTGTGA
7643	db mining	Hs.155462	NM_005915	7427518	minichromosome maintenance deficient (mis5, S. pombe) 6 (MCM6), mRNA /cds=(61,2526)	1	TGTGTAAGAAAAGGCCCATTACTTTT AAGGTATGTGCTGTCCTATTGAGC
7644	db mining		NM_015640		PAI-1 mRNA-binding protein (PAI- RBP1), mRNA /cds=(85,1248)	1	TTGTTGGTAGGCACATCGTGTCAAGT GAAGTAGTTTTATAGGTATGGGTT
7645	db mining		NM_024805	13376184	hypothetical protein FLJ21172 (FLJ21172), mRNA (cds=/138 1169)	1	TTTCTAGCTTTTCCGTGTATCTAAACA CAATTTGCTACACAAGTCACTGT
7646	db mining	Hs.150275	D87682	1663699	mRNA for KIAA0241 gene, partial cds /cds=(0,1568)	1	ACTGTGGCACATGTTTTGATCAGAAA GGTAGTTCTCTTTGCTCTGGTAGT

					Table 8		
7647	db mining	Hs.11039	NM_024102	13129109	hypothetical protein MGC2722 (MGC2722), mRNA /cds=(69,1097)	1	CATCTTCTGCCCTGGTCCCCTTTCTC TTGATGTGGAAAGTCTGAATGCAG
7648	db mining	Hs.102708	NM_015396	7661561	DKFZP434A043 protein (DKFZP434A043), mRNA	1	CGCTCTAATACTGCATTCTGTTTCTC CTTTTGTGCCCTGATTGTAATCCA
7649	db mining	Hs.109646	NM_002493	4505364	/cds=(697,1425) NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17)	1	CTGGAGACTGGAGAAGTAATTCCACC AATGAAAGAATTTCCTGATCAACA
7650	db mining	Hs.142307	AL137273	6807710	(NDUFB6), mRNA /cds=(68,454) mRNA; cDNA DKFZp434l0714 (from clone DKFZp434l0714) /cds=(0,412)	1	TCAGTGTTTCGTTATTCCATATCAGTG GCTTTTACTGTCAAAGATTGTGT
7651	db mining	Hs.16297	NM_005694	5031644	COX17 (yeast) homolog, cytochrome c oxidase assembly protein (COX17),	1	TGCATGAGAGCCCTAGGATTTAAAAT ATGAAATGGTGGTCTGCTGTGA
7652	db mining	Hs.11184	NM_017811	8923387	mRNA /cds=(86,277) hypothetical protein FLJ20419 (FLJ20419), mRNA /cds=(191,907)	1	TGTGCTAAGCCTGATGAAATGTGCTC CTTCAATCTCCATGAAACCATCGT
7653	db mining	Hs.12013	NM_002940	4506558	ATP-binding cassette, sub-family E (OABP), member 1 (ABCE1), mRNA /cds=(117,1916)	1	AAATGATCTCCCTTTATTACCCTCCCA AAGGTTACCAGCGTTTGAATTTA
7654	db mining	Hs.155485	NM_005339	12545382	huntingtin interacting protein 2 (HIP2), mRNA /cds=(77,679)	. 1	ACACACTAATGTAACCATTTTATGAAG GTTGAAGTGGATTTATGCAGGCA
7655	db mining		AW955094	8144777	EST367164 CDNA	1	ATCAGGAGAATGTCAAAGAAGTCCTT TATGTGGATTGCCCGAGCTTCTCT
7656	db mining	Hs.142157			lodestar protein mRNA, complete cds /cds=(30,3518)	1	ATTGTGCCACTGTTTTCCAGCCTGGG CAATACAGTGAGACCCTGTCTCAA
7657 7658	db mining db mining	Hs.1191 Hs.13340	AK025679 NM_003642	10436273 4504340	cDNA: FLJ22026 fis, clone HEP06537 /cds=UNKNOWN histone acetyltransferase 1 (HAT1),	1	CGTCAAAGTCAATCCCAAAACAGATA AGCCCTATGAGGATGTCAGCATCA ACGACTTGCTCAAGAGTAAAGATTAT
7659	db mining		NM_014034	7661591	mRNA /cds=(36,1295) DKFZP547E2110 protein	1	ACTGCTCTGTACAGGAAGCTTGCA TGTTGAGGAAAGGAA
	-				(DKFZP547E2110), mRNA /cds=(192,806)		TCTAAACATGGATTCTGAGTTGTA
7660	db mining	Hs. 123295	AA833793	2906561	od61g07.s1 cDNA /clone=IMAGE:1372476	1	GTGGATGAGTAGGGAGTGGGCGAGA CAGGGACGAGATGAGCAGGGTCAAG
7661	db mlning	Hs.126565	AB020668	4240210	mRNA for KIAA0861 protein, partial cds /cds=(0,2948)	1	GGTGTTCGTGTTAGTGCCAAGATTGC TTCGTTGTAGAGAGAGTTCGTTCC
7662	db mining	Hs.155174		2887434	KIAA0432 mRNA, complete cds /cds=(0,2251)	1	ACTAGAGTCCAGGTAATAGTAGTGGA GATATGTGGAGAGACATGATAGGT
7683	db mining	Hs.116445	AA648776	2575205	ns24d11.s1 cDNA, 3' end /clone=IMAGE:1184565 /clone_end=3'	1	TTCCTGTGTGAGATTTCTCGCCATTC CTCAATTCAACAAATATGCCTTTT
7664	db mining	Hs.124933	AA825303	2898605	oc67e04.s1 cDNA, 3' end /clone=IMAGE:1354762 /clone_end=3'	1	TATACTTTGATCCCTCAGCAAGTTGT CCTCACTGTTGTGTGAACCTGTTT
7665	db mining	Hs,313267	AW295641	6702277	UI-H-BW0-aip-e-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729975 /clone_end=3'	1	TTTCCTGAATACTTTATGACAACTGAG TTTGCCGGGTAGAGTGGCCGTTT
7666	db mining	Hs.313203	AW293882	6700518	UI-H-BW0-ain-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729941 /clone_end=3'	1	AAACTAGAATTCCGGTTTCCCAAGGT GGCTTATGACAACCAGAATCCTTT
7667	db mining	Hs.105488	AA521017	2261560	aa70f05.s1 cDNA, 3' end /clone=IMAGE:826305 /clone_end=3'	1	GGCTTCCCGCCTGTGCAGTCATTTGT ATGTGTTTTATATATTGGAGTGTT
7668	db mining	Hs.125802	AA806833	2876409	oc29b10.s1 cDNA, 3' end /clone=IMAGE:1351099 /clone_end=3'	1	ACAAAATATAAGGTGTGACTTTTGGAT CCTGACTCAAACCAACCAGCTGTT
7669	db mining	Hs.313274	AW295745	6702381	UI-H-BW0-aiw-g-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730834 /clone_end=3'	1	TCAAAATCCGTTACTCTTTCCACAACA ATTGAGGGTAATGGTGTTCAGTT
7670	db mining	Hs.320376	BF512113	11597325	UI-H-BW1-ami-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070302 /clone_end=3'	1	GCCATTCCGGCTTCTCTATTTGAAAA CAGTTACCATATTCCCCCTCAGTT
7671	db mining	Hs.315341	BE675056	10035597	7f01f10.x1 cDNA, 3' end	. 1	ATTTGGTAGAGACGGGGTTTCACCTT ATTGCCCAGGCCATCATGTATCTT
7672	db mining	Hs.320407	BF512394	11597660	UI-H-BW1-amc-f-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069456	1	TGTCATTTGCCCTTTCCCCCATATAT GTAGAATTGGGTCTTTTTCAACTT
7673	db mining	Hs.313347	AW297156	6703802	end /clone=IMAGE:2731329	- 1	ACAGGGAGAGACTACACACAAGCCA ACCTCAATCTCATCTTTATGCCATT
7674	db mining	Hs.123298	AA809468	2878874	/clone_end=3' ob85a10.s1 cDNA, 3' end /clone=IMAGE:1338138/clone_end=3'	1	TCTTCTTTTTGATGTGAATTACTCTTG AAATGCCGGAGAAGGGACAAATT
7675	db mining	Hs.320416	BF512570	11597749	UI-H-BW1-amf-e-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069791	1	AGATAGAGTCATATTCTATTTAGCTTG GGACATGGCAGGTACTCAGTTGT
7676	db mining	Hs.309262	Al440532	4300887	/clone_end=3* CM4-NT0290-150101-684-e05 cDNA	- 1	AGCCTTTTTGGGAGTGAGGGTTTATA TGATGTCTGATTCTGTAATACTGT
7677	db mining	Hs.313338	AW297010	6703646	UI-H-BW0-ajf-d-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731441 /clone_end=3'	1	GCAGCCTGAGCCTGGAATAGATACT TTTTGGTCTTTTGGTTGTAGATGT

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					Table 8		
7678	db mining	Hs.315325	BE646400	9970711	7e86c01.x1 cDNA, 3' end /clone=IMAGE:3292032 /clone_end=3'	1	CCCTCCCTATCTTTTTATGGGTAATTT GATTATACACGGTGCTTGAATGT
7679	db mining	Hs.313172	AW293016	6699652	UI-H-BW0-aih-F04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729239	1	TATGTCTTCTTACCCCAGCACCCCTA ATTTAAAATACAGATCCCTGAGGT
7680	db mining	Hs.313361	AW297413	6704049	/clone_end=3' UI-H-BW0-ais-b-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730208 /clone_end=3'	1	AAAACCTTGACAGTTCATTTCACCAA GCACCTATCAGGTATTTGGCAGGT
7681	do mining	Hs.313365	AW297482	6704118	/clone_etio=3 UI-H-BW0-aja-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730920 /clone end=3'	1	AGTGCCCATGCTGTTTCAGATGCTCT TCTAGCTCCTGGAGATACATCAGT
7682	do mining	Hs.313358	AW297377	6704013	UI-H-BW0-air-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730381 /clone_end=3'	1	TGAGCTTCTGCTAGTAATTCCTTCAG GGGATTTCCTCCATGGCCGTAAGT
7683	db mining	Hs.320474	BF513180	11598359	UI-H-BW1-amj-d-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070115 /clone end=3'	1	GAGGGTGTCTGCTAATGATTTCCGAA AAGTTCTTCAAAACACTCCGAAGT
7684	db mining	Hs.313382	AW297707	6704343	UI-H-BW0-ajh-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731915 /clone_end=3'	1	ACCAGTGTGATGAGTTTTGACAAGAG ACAAAAGGAAAGG
7685	db mining	Hs.125779	AA810831	2880442	ca76d09.s1 cDNA, 3' end /clone=IMAGE:1318193 /clone_end=3'	1	GCTGGTTGTTGCCTTTCAAGACAGCC AACTACCATTTATTCAACAGAAGT
7686	db mining	Hs.313389	AW297882	6704507	UI-H-BW0-aju-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733036 /clone_end=3'	1	AGTCTGTCTATTCTCTTCTCTTTAGCT CTGTCTGTTGCTCAAATTCAAGT
7687	db mining	Hs.313391	AW297905	6704541	UI-H-BW0-aju-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733188 /clone_end=3'	1	GCCAAGGTGAGTCAAAACACTGCTCT TCAGAAAGCAATTATTTGAAAAGT
7688	db mining	Hs.309446	A1492055	4393058	tg12a01.x1 cDNA, 3' end /clone=IMAGE:2108520 /clone_end=3'	1	CATTGTCCCTCCCGCTGTGCTCTCAG GCAATAAATGATTTGATT
7689	db mining	Hs.313311	AW296433	6703069	UI-H-BW0-aiq-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730128 /clone_end=3'	1	GGTCAGAAACAGGCCCACAGAGACT CTGGAGGGTTCTTCCTTTGTGTTCT
7690	db mining	Hs.319887	BF507608	11590906	UI-H-BW1-ana-e-05-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071720 /clone_end=3'	1	TTCAACTGCTTTGGCACTGCCATGGG TACCTGAGGATAAGAGAGATGTCT
7691	db mining		AW293790		UI-H-BI2-ahp-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2727635 /clone_end=3'	1	GGGTTGACTAAATGCACATGGGCTTA TCTTTACCTCTTCCAGAAATGTCT
7692	db mining	Hs.313363	AW297459	6704095	UI-H-BW0-ais-g-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730436 /clone_end=3'	1	TGCATGACCAGAAACACTGCCTGATA CAGTAAGCAGAGGTAGCTGTCTCT
7693	db mining	Hs.320367		11597272	UI-H-BW1-ami-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070074 /clone_end=3'	1	ACCTGCCAGCCAGCCCACACTATAA ACTGTGTGACACCCAAATTTATCT
7694	db mining	Hs.320440			UI-H-BW1-amm-d-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070494 /clone_end=3'	1	GGTTTCTGAGGTGATTCTAATATGCA GTCATGGTTAAGAACCTGTGATCT
7695	db mining	Hs.313374			UI-H-BW0-ajg-e-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731854 /clone_end=3'	1	AAGCCTTGGACCAGCTTCCCGTTTCT CTCTTGTCTCCTGCCAAAAGATCT
7696	db mining		AW297325	6703961	UI-H-BW0-air-a-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730135 /clone_end=3'	1	ACCCAAAGGATGGTGTCTCCTGTCCC AGTTGAAAAGGTTTCTACCTAGCT
7697	db mining	Hs.320420			UI-H-BW1-amf-h-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069925 /clone_end=3'	1	TGGTTGAATACGCAGGAACACCCACA GTACCCAGGGACTAATAAATAGCT
7698	db mining	Hs.118899	AA243283	1874128	zs13g11.s1 cDNA, 3' end /clone=IMAGE:685124 /clone_end=3'	1	TTAGGGCAGTGGAGAATCAGGGTGT ATCTAATAAATTCCTTCATGGAGCT
7699	db mining	Hs.105228	AA489212	2218814	aa57d11.s1 cDNA, 3' end /clone=IMAGE:825045 /clone_end=3'	1	GCAGATGTCTGCGTCATGGTTTATTA CTCCTGTGTTCGTTTCAAGGAGCT
7700	db mining	Hs.297505	BF514865	11600044	UI-H-BW1-anj-f-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082534 /clone_end=3'	1	TGTCTGTATTTGGAGTCCAGTAGTAC ACTGAAAATAATCCCGTAAAAGCT
7701	db mining	Hs.320492	BF513340	11598519	UI-H-BW1-amk-b-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070050 /clone end=3'	1	CTCCCTTCCCACCATACACACACACTCC CAGCTCATTTTGATTCCTTTTCCT
7702	db mining	Hs.304837	AW292802	6699438	UI-H-BW0-aij-f-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729615 /clone_end=3'	1	GGTGAAATTGACTGGGTTCCTCTCCC ACCTCTCTTTCCGTAGCAATTCCT
7703	db mining	Hs.24656	BF507762	11591060	KIAA0907 protein (KIAA0907), mRNA	1	ACTAATTCCCGTGTCTGGCCCTGAAC ATGAAGATATAATGGACGATCCCT
7704	db mining	Hs.320460	BF512975	11598154	/cds=(26,1720) UI-H-BW1-amh-b-06-0-UI.s1 cDNA, 3'	1	TTAAAGGCTCAAACCTACCTCAGACA
7705	db mining	Hs.313384	AW297745	6704381	end /clone=IMAGE:3069659 /clone_end=3' UI-H-BW0-aiy-b-10-0-UI.s1 cDNA, 3'	1	CTGCTCTACCCATCCCCATCCCCT CCCTTTGTGAGAAGAAGCAGGTTTCC TTTCCTATGGATTGATGTGACCCT
					end /clone=IMAGE:2730954 /clone_end=3'		THOU AND AND TO A DO T

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7706	db mining	Hs.105105	AA419402	2079198	zu99a12.s1 cDNA, 3' end	1	TTCTACCCATCACACAGATTCTTCCA CTTAATAAAATCCATCACCTACCT
7707	db mining	Hs.123180	AA805419	2874169	/clone=IMAGE:746110 /clone_end=3' oc13g03.s1 cDNA, 3' end /clone=IMAGE:1340788 /clone_end=3'	1	TCATTACTGTTGTGAAGGCTCTTCAA GAGAGAAAGATGAAGCTGAAACCT
7708	db mining	Hs.297396	BF515183	11600450	UI-H-BW1-anl-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082728	1	GCTGTCCGTGAAAGCACTCTCAAGTC AGGAACTGAACTAAGAACTTTACT
7709	db mining	Hs.334992	AI084211	3422634	/done_end=3* RST20881 cDNA	1	CTCCTGTAATCCCAGCACTGGAGCTT
7710	db mining	Hs.313273	AW295743	6702379	UI-H-BW0-aiw-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730830	1	GCAGTGAGCCAAGATCATGCCACT TTGGTCACCACACCTGGGTGTCTGAA TGTCTTGTCCTTCTAAAGGTAACT
7711	db mining	Hs.319891	BF507631	11590929	/clone_end=3' UI-H-BW1-ana-h-01-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071856	1	GCAACAATTCTTTGGAAAGTGACTCT CTAGGGTGCGGAGAATGGTGTGAT
7712	db mining	Hs.320422	BF512614	11597793	/clone_end=3' UI-H-BW1-amg-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069622	1	TCATCTCTGTAGGTCTTCCTAATCCTA TGCGGAGCCAAATATAGACGGAT
7713	db mining	Hs.319872	BF507414	11590721	/clone_end=3' UI-H-BW1-amz-a-11-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071517	1	CTTTGTATTTCAAAGAAAGTAGCCCC TTGGCTCTGATATTAGTTGCAGAT
7714	db mining	Hs.264120	Al523641	4437776	/clone_end=3' 601436078F1 cDNA, 5' end /clone=IMAGE:3921187 /clone_end=5'	1	TTTAGGAGCTGACCATACATGATGAG TGATACAGCCTGTACTTTGCTCAT
7715	db mining	Hs.105284	AA491263	2220436	aa49d04.s1 cDNA, 3' end /clone=IMAGE:824263 /clone_end=3'	1	ACTGG GATGAGATGAGATTCAAGGCA CTTTTGGAGGGTGTAGCTAGCCAT
7716	db mining	Hs.124376	AA831043	2904142	oc58h02.s1 cDNA, 3' end /clone=IMAGE:1353939 /clone_end=3'	1	AGGCTGTTGCTGCACGGGCTTTTCAA AAGCGACTCATTATGAAGAAGAAT
7717	db mining	Hs.309144	Al384035	4196816	td05c02.x1 cDNA, 3' end /clone=IMAGE:2074754 /clone_end=3'	1	GCACTCCAGCCTGGGCAACAAGAGC GAAACTCTGCCTCCAATAAATAAAT
7718	db mining	Hs.301325	BF514004	11599183	UI-H-BW1-amv-e-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3071311 /clone end=3'	1	CGGGCGGTGGCGGCTGCCTGGGAG AAGATGAATCTTTCATGAGTGATTTG
7719	db mining	Hs.319904	BF507742	11591040	UI-H-BW1-anc-f-02-0-UI.s2 cDNA, 3' end /clone=IMAGE:3072122 /clone end=3'	1	GATGGAACTCAAGGTGCTTTACGCTT TCCTCAGTCTTACCAGGAGGCTTG
7720	db mining	Hs.320092	Al392740	4222287	tg23f02.x1 cDNA, 3' end /done=IMAGE:2109627 /done_end=3'	1	ACCAACCCTATGGACAACTTGATCTT GAACTTCTAGCTTTCAGACCTGTG
7721	db mining	Hs.313371	AW297578	6704214	UI-H-BW0-ajg-b-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731708 /clone_end=3'	1	AATGTAGCTGACATTGGAGCCACCGC CCATAGAAGAAGGCTAAAACTGTG
7722	db mining	Hs.320444	BF512784	11597963	UI-H-BW1-amm-h-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070698 /clone end=3'	1	CTTCACTGACGATCTGAGACACTAGG CAGGTTGGAAAGGGTGGAGTGGTG
7723	db mining	Hs.320473	BF513155	11598334	UI-H-BW1-amj-b-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070013 /clone end=3'	1	GCCCCTGGTGGTTGGAAAAGTGTTCT GAATCCAATAAAAGGAAAGCGGTG
7724	db mining	Hs.320419	BF512597	11597776	UI-H-BW1-amf-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069921 /clone end=3'	1	CAACAGTGGCAAGAGTAGCCAGCCC ATAGGACGGAATGAAAATCAAGGTG
7725	db mining	Hs.320365	BF512157	11597260	UI-H-BW1-ami-b-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070026 /clone end=3'	1	CATCCTTAGATGCCAGTCTTCACTTT GGGTATTTTCCTGCCTCCTCAGTG
7726	db mining	Hs.299471	BF513893	11599072	UI-H-BW1-amq-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070874 /clone end=3'	1	ACCAACAGTACCGTTATTGCCACCAC AAGTAAACCAGTCCCTCACTTCTG
7727	db mining	Hs.313368	AW297544	6704180	UI-H-BW0-aja-g-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731200 /clone_end=3'	1	AGGCTAAATCAGAGCTTTCCTCCCCA GATAAAGGAAATTTTCCCTCCCTG
7728	db mining	Hs.105170	AA481410	2210962	zv02g12.s1 cDNA, 3' end /clone=IMAGE:746374 /clone end=3'	1	AACTTCCAGAGGCAGGAGATTAGACA GGGATGACAGTTAAGGGGTTACTG
7729	do mining	Hs.313251	AW295130	6701766	UI-H-BW0-ait-h-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730495 /clone end=3'	1	ACCTCTTCGTTGTATTTTACCTTTCAC TTACAAACAAGCTCATGCCACTG
7730	db mining	Hs.297392	BF514201	11599380	UI-H-BW1-ani-d-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082401 /clone_end=3'	1	GATCAAAACAAGGTCCTTGACTTTTT GCAGGGGCAGCCTGGCAATCAATG
7731	db mining	Hs.122417	AA761212	2810142	nz20c03.s1 cDNA, 3' end /clone=IMAG E:1288324 /clone_end=3'	1	CCTAAATGTTGTCCCTCAGAGATGCA CAGATGTATATGGGTAAGGAAATG
7732	db mining	Hs.297469	BF512785	11597964	UI-H-BW1-amm-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070700 /clone_end=3'	1	CCAACCATAGTCATGAAGCTGCTTCT GTTCCCAATGCAATCCCATTGTGG
7733	db mining	Hs.313275	AW295750	6702386	UI-H-EW0-alw-h-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730868 /clone_end=3'	1	GCTTTTCAATGCTTCCGAAACTGAGT GCTAACAGGGGCAATTAGTGCTGG

					Table 8		
7734	db mining	Hs.313173	AW293031	6699667	UI-H-BW0-aih-g-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729299	1	AGTTCTTGTAACAGTTAAAACTTTCTT GCCAGCTCTCAGGTTATCACTGG
7735	db mining	Hs.320386	BF512295	11597474	/clone_end=3' UI-H-BW1-amb-e-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069389	1	GTGTGTAAATGAGTGTCAGATCTTTT CTTGAAAACAGGTTTGGATTGGGG
7736	db mining	Hs.320429	BF512664	11597843	/clone_end=3' UI-H-BW1-amg-f-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069844	1	AGGGTCCACAAGGAGAATATTTTCTT AAAGTAACTCCCTGATTTGCGGGG
7737	db mining	Hs.123352	AA811133	2880744	/clone_end=3' oa98b10.s1 cDNA, 3' end /clone=IMAGE:1320283 /clone_end=3'	1	GCTCCCCTATGCCTGTGTAGCAGAAT CTAAAAGATAATCATGTGAACGGG
7738	db mining	Hs.320389	BF512323	11597502	UI-H-BW1-amb-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069497 /clone end=3'	1	TTGTCTTGTTTCTTTTATCTCCCCTAT GTTTCATCTTAGTGCAGGCAGGG
7739	db mining	Hs.120563	AA741116	2779708	nz04f08.s1 cDNA, 3' end /done=IMAGE:1286823 /done_end=3'	1	ACAGTTGCCTTTGAGATTCCTGTATTT CTGCATGAATAAATCCATAAGGG
7740	db mining	Hs.320373	BF512098	11597310	UI-H-BW1-ami-f-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070222 /clone_end=3'	1	GTCCTTGGAAGGTAACACTTGTGATT GGAACCACTCTTCAAGCTGAACGG
7741	dib mining	Hs.320490	BF513327	11598506	UI-H-BW1-amk-a-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069996 /clone end=3'	1	ATTCATTCATTCATTCAACAAGCACTT AAAAACAATGCCTGTGTGCCAGG
7742	db mining	Hs.313290	AW296074	6702710	UI-H-BW0-alu-h-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730852 /clone_end=3'	1	CACACCCAGCCCCATTCACAAAGGAC TATAAAATCTACACCCCAGTCACG
7743	do mining	Hs.320390	BF512330	11597509	UI-H-BW1-amb-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069537 /clone_end=3'	1	GGCATAGTAGTGCTAAACAGAGGTG GAAGTAGTGAAGGGAGTTTTGAACG
7744	db mining	Hs.297397	BF507606	11590904	UI-H-BW1-ana-e-02-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071714 /clone_end=3'	1	CTAGTCCTGCCCCCACCTCCCCAAGT ATTACCCCTCCTAAGTCCTGCTAG
7745	db mining	1101202	Al373161	4153027	qz13a01.x1 cDNA, 3' end /clone=IMAGE:2021352 /clone_end=3'	1	AGATAAGCAGGATAAACAAGACAGGT TGGATTGTGATCAGCTCTATGGAG
7746	db mining	Hs.343303		11598501	UI-H-BW1-amk-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069986 /clone_end=3'	1	GATGGCTAGGACAAGATGATTTACAA GAGCGTGGCGGGGAGGGACGGCGAG
7747	db mining	Hs.301870	BF507614		UI-H-BW1-ana-f-03-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071764 /clone_end=3'	1	CCGTGTCTGGATTGTGTGTCTTACTT CTAAAGGTGCACATACTTCATAAG
7748	db mining		AW452510		UI-H-BW1-ame-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069598 /clone_end=3'	1	GTATCTCTGCACCTCACTACTACCCT TCACTCCTTGGAGACCTGGGCAAG
7749	db mining	Hs.320387			UI-H-BW1-amb-e-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069401 /clone_end=3'	1	AACACACCACCAAACATTCTTCCCAT CCTTCTTCACCAACCA
7750	db mining	Hs.122854	AA292626	1940611	zs57h08.r1 cDNA, 5' end /clone=IMAGE:701631 /clone_end=5'	1	ACAATTGGAGTTGGGGCTGTCACCAC CTGAAGTGTGTCAACCACAGAAAG
7751	db mining	Hs.300488	AW453029	6993805	UI-H-BW1-ama-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069306 /clone_end=3'	1	TTAGGGCAAAAGTCCTAGTGGCGGC AGCTTTCTTGTCTAGACCCTGGTTC
7752	db mining	Hs.335081	Al380942	4190807	tg18c08.x1 cDNA, 3' end /clone=IMAGE:2109134 /clone_end=3'	1	AGTGATGCTTGCCTTTTCGCTTTCCT AAAGATGTCATTTGAAAACAAGTC
7753	db mining		AW452916		UI-H-BW1-amd-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069267 /clone_end=3'	1	CCCAGCTTCATTAATGTGAATGGTGG CAGACACCTCTAGCTATAGAGCTC
7754	db mining	Hs.309486		4438094	/clone=IMAGE:2116841 /clone_end=3*	1	GAGCCAAGATTGGGCCACTGCACTC CAGCCTGGGTGACAGAGTGAGACTC
7755	db mining	Hs.303926	Al084223	3422646	oy72g05.x1 cDNA, 3' end /clone=IMAGE:1671416 /clone_end=3'	1	GAGCCGAGATTGCATCACTGCACTCC AGCCTGGTCAACAGAGCGAGACTC
7756	db mining	Hs.313170	AW292942	6699578	UI-H-BW0-aig-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729252 /clone_end=3'	1	TTCAGTCATGCAGCAACATCCGCTTA ATGCCTCCTAAGTGCAGAACACTC
7757	db mining	Hs.313795	AW452553		UI-H-BW1-ame-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069788 /clone_end=3'	1	GGTCCTCTCTCTCTCTCCCTAG TAACTAACCACCAAAGCCTAAATC
7758	db mining	Hs.319883			end /clone=IMAGE:3071079 /clone_end=3'	. 1	TIGITIGITIGITTATITATITATITIG AGGCAGCGTCTTGCTCTGTTGC
7759	db mining	Hs.320476			UI-H-BW1-amj-e-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070155 /clone_end=3'	1	TGCCATCTTTACATCTAATCAAGAGG TAGAGCTTCCCCTGGTGTTCCTGC
7760	db mining	Hs.313828	AW453000	6993776	UI-H-BW1-ama-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069200 /clone_end=3'	1	TGCTCTGCTCTTCCCAAATCAAGGAA TGTAGATCTTGCTAACAGAACTGC

					Table 8		
7761	db mining	Hs.120251	AA731388	2753542	nz86f07.s1 cDNA, 3' end /clone=IMAGE:1302373 /clone_end=3'	1	TGGCACCAACTTACACTTCCAGAAGA GAGTGGTTCAGGAAATTACTATGC
7762	db mining	Hs.313392	AW297908	6704544	UI-H-BW0-ajn-a-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732071	1	AACTITGGGAAGTGAGACTCTGTCTT GGGTTTTTGATAATAAATGTGGGC
7763	db mining	Hs.343320	BF512697	11597876	/clone_end=3' UI-H-BW1-amm-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070346	1	CCGAGAAAGTACGGCTGGAGCGGAC TGGGGAGACGGAAATATTGAGTCGC
7764	db mining	Hs.304176	Al540182	4457555	/done_end=3' td10f04.x1 cDNA, 3' end /done=IMAGE:2075263 /done_end=3'	1	CGAAGAAAGAATTGGATGCAGAATTG TTGCCTAACCTGGGTGACAAGAGC
7765	db mining	Hs.320425	BF512629	11597808	UI-H-BW1-amg-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069700 /clone_end=3'	1	AGTGCCTGTGATTCCACCCCCTTACC TCCCACTCAAGTGACAATGTAAGC
7766	db mining	Hs.313236	AW294711	6701347	UI-H-BW0-aim-b-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729806 /clone end=3'	1	AGAAAGTTAGGAGTCGGCAACCTTAA GGAGGAGTTTCCTATCATCTCTCC
7767	db mining	Hs.313379	AW297666	6704302	UI-H-BW0-ajh-c-02-0-ULs1 cDNA, 3' end /clone=IMAGE:2731755 /clone_end=3'	1	TGTCACAAAGATGAAGCAAGGTGGCT CAGGGAACGTGCTCAGAAACCTCC
7768	db mining	Hs.123341	AA810927	2880538	oa77d07.s1 cDNA, 3' end /clone=IMAGE:1318285 /clone_end=3'	1	GCAAAGTGAAAGTTTTCCCTTTGGCC CTAAAATATGAAAGCAAAGC
7769	db mining	Hs.313208	AW293991	6700627	UI-H-BW0-aik-h-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729726 /clone_end=3'	1	CCCTGTCCATCTTTTCCTGTTCCTATC
7770	db mining	Hs.123344	AA811024	2880635	oa82g05.s1 cDNA, 3' end /clone=IMAGE:1318808 /clone_end=3'	1	CCACGGAGGGCTCCCCATCTAAAGG GAGTTTAATAAACAAAGGAATGGCC
7771	db mining	Hs.320450	BF512839	11598018	UI-H-BW1-amu-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE;3071322 /clone_end=3'	1	CAATTGGTACATTCTCGGCAAACCCT TGCCCACAATTTCCTCAGGAAGCC
7772	db mining	Hs,313369	AW297549	6704185	UI-H-BW0-aja-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731214 /clone_end=3'	1	AGGGTGTCCCTGTGATTTTTAAATTC ACTATCTAGCTGTCCCTATCCCCC
7773	db mining	Hs.297527	BF515924	11601103	UI-H-BW1-ace-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3084001 /clone_end=3'	1	CACCTCACCTCCCAACCCACCCC
7774	do mining	Hs,297513	BF515498		UI-H-BW1-ann-g-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082950 /clone_end=3'	1	GAGAATTCAAATTAAATGCAGAGTCC TAGGCCCACCCTGGCATACCACCC
7775	db mining	Hs.105218	AA488881	2218483	aa55f06.s1 cDNA, 3' end /clone=IMAGE:824867 /clone_end=3'	1	ACAACCAATGCCTCACACTTAAGCTC CTAGAAGTCACTAGGGACCAGACC
7776	db mining	Hs.309447	Al492062	4393065	tg12a11.x1 cDNA, 3' end /clone=IMAGE:2108540 /clone_end=3'	1	GCCCTCACCAGAATTCAATCATGCTG GCACCTTATCTTGGACTTTCAACC
7777	db mining	Hs,309483	Al523758	4437893	tg94e10.x1 cDNA, 3' end /clone=IMAGE:2116458 /clone_end=3'	1	AGGGTAAGAGTTCCAGACCTGACTG GACAATAAAGTGAGACTGTCTCTAC
7778	db mining	Hs.343333	BF515310	11600412	UI-H-BW1-ank-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082577 /clone_end=3'	1	CTCCGTCTGCCGCCTCCGTAGCCAC AGCGACTTTGGAAGTGATATTTGAC
7779	db mining	Hs.309687	Al401187	4244274	tg26h10.x1 cDNA, 3' end /clone=IMAGE:2109955 /clone_end=3'	1	CCCTGGAGAAGGAGGGTGATTTATTT TCAACTTTCTGATTTACCACCGAC
7780	do mining	Hs.314730	AI523958		tg98f08.x1 cDNA, 3' end /clone=IMAGE:2116839 /clone_end=3'	1	GATTGTTTGAGCCTGGGAGTTCCACA CCAGCCTGGGCTACATAGGGAGAC
7781	db mining	Hs.313337	AW297006		UI-H-BW0-ajf-c-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731409 /clone_end=3'	1	CTGCTCTAGACTGAGCACAGCCACTG ACAGGTGACCTTCAGAATCCTCAC
7782	db mining	Hs.116455	AA649141	2575570	ns32g12.s1 cDNA, 3' end /clone=IMAGE:1185382 /clone_end=3'	1	ACCCCTGCTTTACTGTGACAGACATA TAGTTTGTCATACATAAAACCCAC
7783	db mining	Hs.123313	AA810089		od12f12.s1 cDNA, 3' end /clone=IMAGE:1367759 /clone_end=3'	1	ACCTAACAGAAATTTGGATTCGGGTT GTCTAAATACACCCTGGTGGGTTA
7784	db mining	Hs.319868			UI-H-BW1-amx-o-04-0-UI.s1 cDNA, 3' end /clone=IMAGE;3071239 /clone_end=3'	1	GCCTTTCCCACCACAGGTTTATGTGA TTCCCTGCCCTACCCTTACCATTA
7785	db mining	Hs.123342			oa73g11.s1 cDNA, 3' end /clone=IMAGE:1317956 /clone_end=3'	1	TCCCATTGCATGTCCCGTATATTGAA AGCTGCCTCTACTTCTCTCTGGTA
7786	db mining		AW296061		UI-H-BW0-aiu-g-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730802 /clone_end=3'	1	GGCAGGGGATGAACCAGATAATTTCC AGCCCTTCTTGGTAGCTCTTCGTA
7787	db mining	Hs.308998	Al356553	4108174	qz27h12.x1 cDNA, 3' end /clone=IMAGE:2028167 /clone_end=3'	1	GCTTAGGAGTTTTGGGACCAGCCTGG GTAACATAGTGAAACCCTGTCTCTA

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					Table 8			
77 8 8	do mining	Hs.313328	AW296796	6703432	UI-H-BW0-ajb-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731115	1	TTGCAGCTATTTTCAAGTTGTAAGAAA TGAACTTGCAACACATAGGGCTA	
7789	do mining	Hs.320462	BF512986 1	1598165	/clone_end=3' UI-H-BW1-amh-c-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069707	1	TCTCTTGCCACAGGGATTTCCTCCAA GCTGGAATCACCATTTCCTTCCTA	
7790	db mining	Hs.297514	BF516300 1	1601479	/clone_end=3' UHH-BW1-anz-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3084010 /clone end=3'	1	CCCACCCACCAGTAGGTTGTGATTCA ACTGAACCATTTCAGGAGCACCTA	
7791	db mining	Hs.124358	AA830650	2903749	oc52g02.s1 cDNA, 3' end /clone=IMAGE:1353362 /clone_end=3'	1	GAACCCAGCTAAGCCACACCCAGATT CTGACCCAGGGATACTCTGAAATA	
7792	db mining	Hs.313345	AW297163	6703789	UI-H-BW0-ajd-a-04-0-UI.s1 cDNA, 3' end /clone=tMAGE:2731279 /clone_end=3'	1	GTGTGTGCTGGCGTGCCTTATAGGT GTGCGTGTTTCCCTGTCAGTTTTGA	
7793	db mining	Hs,320484	BF513246 1	1598425	UI-H-BW1-amo-b-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070426 /clone_end=3'	1	AGGAAAACTCAGAAATAATTTCTGCC CCCTGGATTCTCTAAGATTTGTGA	
7794	db mining	Hs.105130	AA482030	2209708	zu98g04.s1 cDNA, 3' end /clone=IMAGE:746070 /clone_end=3'	1	GTGGAAAGAATCCTACAACGAACACT ATTAAAGTCTGCACCTAGATCTGA	
7795	db mining	Hs.104176	AA214530	1813155	zr92a06.s1 cDNA, 3' end	1	GGCCTAGGTTCCAGCATTCAGTCATC	
7796	db mining	Hs.121118	AA721101	2737236	/clone=IMAGE:683122 /clone_end=3' nz67e01.s1 cDNA, 3' end /clone=IMAGE:1300488 /clone_end=3'	1	AAGTCTTGTTACAGAAATAAATGA CCCCATTTGGAGTCTAGTCAAAACAG CAGCTTCTTTGAGTTACCATTGGA	
7797	db mining	Hs.313313	AW296455	6703091	UI-H-BW0-aiq-c-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730224 /clone end=3'	1	AAGGCTTGTAACTGTAGGCCCTTGTA CTACACTGTGCTATACCTGGTAGA	
7798	db mining	Hs.335116	Al524072	4438207	th01d07.x1 cDNA, 3' end /clone=IMAGE:2117005 /clone_end=3'	1	CACTTTGGGAGGCAGAGGTGAGCAG ATCACTTGAGGCCAGGAGTTTGAGA	
7799	db mining	Hs.309130	Al382229	4195010	td04d04.x1 cDNA, 3' end /clone=IMAGE:2074663 /clone_end=3'	1	GGATCACTTGAAGCCAGCAGTTTGAG ACCAGCCTGGGCAATAAAATGAGA	
7800	db mining	Hs.297504	BF514819 1	1599998	UI-H-BW1-anj-b-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082338 /clone_end=3'	1	TCAGTTGTGATGGGATTTCTTGATGG ATGAGATGTGTCGTGTGACAGAGA	
7801	db mining	Hs.297473	BF513074 1	11598253	UI-H-BW1-amn-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070445 /clone_end=3'	1	CCTCCTAGAACTGGAACCAAGACTGC TCCATCAGAGTTAAAGGTGTAAGA	
7802	do mining	Hs.313168			UI-H-BW0-eig-d-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729144 /clone_end=3'	1	GCTCACCCTTGCACCTCCTTCCCAAA TCTGCTGTCACATTTTCTCAAAGA	
7803	do mining	Hs.319885			UI-H-BW1-ana-b-03-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071572 /clone_end=3'	1	TTCCTGTCTCCATGTTGTGGTCAAGA TTGCCATTTGCTTCCTGAGTTTCA	
7804	db mining	Hs.320411		1597693	UI-H-BW1-amc-h-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069570 /clone_end=3'	1	CTGGTTCTAGTGCAGTCTCCTCACTT TCCTGGTGTTTGGTTTATCTTTCA	
7805	do mining	Hs.116501			ns40b05.s1 cDNA, 3' end /clone=IMAGE:1186065 /clone_end=3'	1	TGACATGATTACCTGACTGATGTTTC TCCTCCATTAGACTGAATGCTTCA	
7806	do mining				UI-H-BW1-amm-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070440 /clone_end=3'	1	TGGCAAAAAGCCTAACACTGACTCAT CCCATTCTATCAGCACAAACTTCA	
7807	db mining	Hs.319888			UI-H-BW1-ana-e-12-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071734 /clone_end=3'	1	GTTTACAAGGGATACTAGTTCCTGGA GGGACGAAGGAGGCTCTGTTTGCA	
7808	db mining				UI-H-BW0-ajm-g-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732352 /clone_end=3'	1	TCCTCAACTCGGAGATTCCTGTATGG AGAGAATCAATTTCTATATTTGCA	
7809	db mining	Hs.120738			nx99c09.s1 cDNA, 3' end /clone=IMAGE:1270384 /clone_end=3'	1	ACATTTCTTAGGTGTGTAGTGGTGAA GGAAAATAGTGGAAGATGTCTGCA	
	db mining	Hs.320404		•	UI-H-BW1-amc-b-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069264 /clone_end=3'	1	TCAGGAGGCTTGAAAAGACTCAAGGT TTCTACACTATGGGAAATAAGGCA	
7811	db mining	Hs.319880			UI-H-BW1-amr-c-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070831 /clone_end=3'	1	GTTTCACTTGTGATACTAACTATTGT TTTTCTCCCCCATGCCAAGAGCA	
	db mining	Hs.320371			UI-H-BW1-ami-f-05-0-UI.s1 cDNA, 3' end /clone=iMAGE:3070208 /clone_end=3'	1	AGCCAAGGGAGCATATTATTCTCTTA TTTTAAACCTCTCCGTAGGCAGCA	
	db mining	Hs.307837		3308774	oy78h09.x1 cDNA, 3' end /clone=IMAGE:1672001 /clone_end=3'	1	AGAAGGACCCCTGGTTGAGAACCAC GGTTGTATAGAAAGGAATTGAAGCA	
7814	db mining	Hs.124383			oc85b04.s1 cDNA, 3' end /clone=IMAGE:1356463 /clone_end=3'	1	TTGACTGCCATAGCCAAGAGTTAATA TAGTTGCGTTTTCTTAAGGAAGCA CTTACTGTGCTTTTAGGTTTTGTTGCT	
/815	db mining	Hs.123304	AV4808012	∠d/9U/8	nz99b08.s1 cDNA, 3' end /clone=IMAGE:1303575 /clone_end=3'	1	TTCTGTCTGTATGCTATGTTCCA	

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7816	db mining	Hs.123368	AA811539	2881150	ob45d08.s1 cDNA, 3' end /clone=IMAGE:1334319 /clone_end=3'	1	TGCAGTTAGGAGTGTGGACACTCTGC CCATCTCCATTGAATTAAATTCCA	
7817	db mining	Hs.313176	AW293164	6699800	UI-H-BW0-aii-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729448	1	ACTTGGGTTCTATCCCCACGATAACT TGTTATGTATATGCCAATATCCCA	
7818	db mining	Hs.313171	AW292976	6699612	/clone_end=3' UI-H-BW0-aih-b-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729055	1	AGCTAGAAAATGTCCCTTTTTCTTCTT TGGAGGTCTTTAACCAAGGCCCA	
7819	db mining	Hs.343308	BF508886	11592184	/clone_end=3' UI-H-BI4-aos-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3085732	1	ATCACCAATCTTATTTAGCACTGTGG ATGCCGTTTTGCAAATGTCACCCA	
7820	db mining	Hs.320468	BF513104	11598283	/clone_end=3' UI-H-BW1-amn-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070555 /clone end=3'	1	TGACTTAAGGTTGGAATATCTCCTAC TACTCCCCTGTCCTCCTTGGACCA	
7821	db mining	Hs.120585	AA743221	2782727	ny21c06.s1 cDNA, 3' end /clone=IMAGE:1272394 /clone_end=3'	1	TGTGGTTTGCAATGGTTTACTGATGA GACAGCAAAAATGAGACAGGACCA	
7822	db mining	Hs.297468	BF513126	11598305	UI-H-BW1-amn-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070649 /clone_end=3'	1	TGGCGAGCCAGTCTCTGGATGGGAT TCTGATCAACAGAAGTTCTCATACA	
7823	db mining	Hs.313205	AW293932	6700568	UI-H-BW0-alk-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729426 /clone end=3'	1	TGCCCATCCTTTGCTGTTTTTCTCTTT CAGTCATGGCCTATTTGGAGACA	
7824	db mining	Hs.343329	BF515646	11600825	UI-H-BW1-anu-d-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3083555 /clone end=3'	1	CTCAACCTTGGCCCTAAACTAACAGT GACAGGGAGTTCCCCAGCCTCACA	
7825	db mining	Hs.319906	BF507755	11591053	UI-H-BW1-anc-g-07-0-UI.s2 cDNA, 3' end /clone=IMAGE:3072180 /clone_end=3'	1	TCCTGACCGTTGACAGAGAGCTTTTA CAGAAGTCTTAGGCAGTACACACA	
7826	db mining	Hs.320465	BF513053	11598232	UI-H-BW1-amn-a-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070355 /clone_end=3'	1	AGTGTGTGGCACCCAGGGATCACTG TATGAGAATTTCCTGAACAACAACA	
7827	db mining	Hs.320430	BF512667	11597846	UI-H-BW1-amg-f-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069850 /clone_end=3'	1	GCTGTAAGTCCCTTCCTTACTCATCT TCCCTCTCAAATACAACAACAACA	
7828	db mining	Hs.120718	AA748539	2788497	ny05h12.s1 cDNA, 3' end /clone=IMAGE:1270919 /clone_end=3'	1	GCCAGTTGGCACCATTTATGAAACAC ACCACCTTGTAACCACTGAATTAA	
7829	db mining	Hs.320472			UI-H-BW1-amj-b-02-0-UI.s1 cDNA, 3' end /clone=iMAGE;3070011 /clone_end=3'	1	TCAACCTAGCACAGTGCCTGGCTGAT AGGTGTTGAATATTTCCACTCTAA	
7830	db mining	Hs.319899	BF507695	11590993	UI-H-BW1-anb-h-05-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071865 /clone_end=3'	1	GCAACCCTCTGCCCCTGCAAAGAGAT ATTGTGACAAAGATATTCACTGAA	
7831	db mining	Hs.124932		2898575	oc67a02.s1 cDNA, 3' end /clone=IMAGE:1354730 /clone_end=3'	1	TAACATTCCTGGCACAGTCCCTGGCA TAGGGTAGATAATAAATGGTGGAA	
7832	•		AW297308		UI-H-BW0-aji-h-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732020 /clone_end=3'	1	TCTCTAACCATCAAGGAAGGTCAAGG GCCATGTATCTCTTTTAGGGAGAA	
7833	db mining	Hs.127178		3096753	oc10g07.s1 cDNA, 3' end /clone=IMAGE:1340508 /clone_end=3'	1	TTCCACAAACTCAGGTGTGCAAGAAA CAATGCATTACTTTATTTTCAGAA	
7834	db mining	Hs.320445			UI-H-BW1-amm-h-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070702 /clone_end=3'	1	CAGGAGTTTGAGACCAGCCTGGGCA ACATAGTAAGTCTCCATCTCTTCAA	
7835		Hs.319902			UI-H-BW1-anc-b-02-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071930 /clone_end=3'	1	TCCCTAGTCCTGGAGACTCGGGAACT AAAACAATCAATTCCCCTGAGCAA	
7836	db mining	Hs.104348		1886301	zs08a06.s1 cDNA, 3' end /clone=IMAGE:684562 /clone_end=3'	1	TCCTCTTCATTGGAGACCCCTCCCTG TCACAGCACAATGTGGGTAATAAA	
7837	db mining	Hs.320442		11597940	UI-H-BW1-amm-f-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070598 /clone_end=3'	1	CAGAACAAGGCCCACAGTGTGAAAG GTGCTGCTGAACAAAGATAAATAAA	
7838	db mining	Hs.320470			UI-H-BW1-amj-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069983 /clone_end=3'	1	GAGTCAGCAACACTGGTCCTCTTGCC TTGGTTGATGCTTTTGAACTGAAA	
7839	db mining	Hs.300359	BF516423	11601602	UI-H-BW1-aob-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3084512 /clone_end=3'	1	TAAGGATGTATCCCTATGGGCAGGAA ACCCAATTCTAAGAAACTTACAAA	
7840	do mining	Hs.309152		4222517	tg22d05.x1 cDNA, 3' end /clone=IMAGE:2109513 /clone_end=3'	1	GCCACTGCACTCCAGCCTGGGCAAC AGAGCGAGACCTTGACTCTTTAAAA	
7841	db mining	Hs.122448			nz31e08.s1 cDNA, 3' end /clone=IMAGE:1289414 /clone_end=3'	1	CACAACACCCAAAAGGCTGCATTGCA TAACATGTATTTGTTGAATGAAAA	
7842		Hs.319874	BF507452		UI-H-BW1-amz-e-06-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071699 /clone_end=3'	1	GGGGTCCTTGCTCACAGAGCTCCCA AGATGGTGGTGGGCCACTTCCAAAA	
7843	db mining	Hs.104177	AA214542	1813167	zr92b09.s1 cDNA, 3' end /clone=IMAGE:683129 /clone_end=3'	1	TCCCTCTATAGGTAAAAGACCTGTTT GTCTGAAATGTGTGGAACCTGTCT	

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7844	db mining	Hs.104182	AA521405	2261948	aa68c06.s1 cDNA, 3' end /clone=IMAG E:826090 /clone end=3'	1	GCTGCCGTGTCTTTTGGCATTTTCAG CATGACTATATGTTTTTTGTAATGT
7845	db mining	Hs.255522	AW296182	6702818	UI-H-BI2-aia-c-01-0-UI.s1 cDNA, 3' end /clone=iMAGE:2728680 /clone_end=3'	1	CCGAAGGCCCGTGTGGCGCTTCTCC TATTCTGTAGAGTGGTAGTTTGTTT
7846	db mining	Hs.124926	AA765668	2816906	oa04f02.s1 cDNA, 3' end /clone=IMAGE:1303995 /clone_end=3'	1	AAAGAGGTAAACGCAAGTTCTCTTT GTAGGTCGGGCTACAGGTGACTTT
7847	db mining	Hs.320388	BF512314	11597493	UI-H-BW1-amb-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069453 /clone_end=3'	1	TGGTTCTCAGCCTGGGTGAACAGAG AAGGGGTCTAATTTGGTCTTTTGTT
7848	db mining	Hs.123161	AA807319	2876895	oc38b01.s1 cDNA, 3' end /clone=IMAGE:1351945 /clone_end=3'	1	TGTTCTTGGCACCCTGCACTGTCAGG CTATATCATTTCTGTTTGTTTCTT
7849	db mining	Hs.120608	AA743877	2783228	ny25b04.s1 cDNA, 3' end /clone=IMAGE:1272751 /clone_end=3'	1	TCTCATTTTCTTTTCCTAGCTGTGATG CAAAGTGTCAGTGGTCCCATCTT
7850	db mining	Hs.120554	AA741010	2779602	ny99a10.s1 cDNA, 3' end /cjone=IMAGE:1286394 /clone_end=3'	1	TGTCCAACCTTCCTTTTGCTACAAAC AAAGAATGCCTAGGGATTCAACTT
7851	dib mining	Hs.330148	BE676227	10036768	xm80f05.x1 cDNA, 3' end /clone=IMAGE:2690529 /clone_end=3'	1	CAAGTGGCCTTGGTGTTTTAAATCTTG CCCTAAATTGTAACTCACATGATT
7852	db mining	Hs.120259	AA731522		nw59h09.s1 cDNA, 3' end /clone=IMAGE:1250945 /clone_end=3'	1	ACCAACCAGTGGTGTGCTGGAGCTG TCTCATACTATCTTGAGAGTCCATT
7853	do mining	Hs.124333	AA829233	2902332	od05a10.s1 cDNA, 3' end /clone=IMAGE:1358298 /clone_end=3'	1	AGCACTTGCTTTGTTCCAGACATTGT CCTTAGCTCCTTTCTTGTGTAATT
7854	db mining	Hs.124281	AA825840	2899152	od59d02.s1 cDNA, 3' end ' /clone=IMAGE:1372227 /clone_end=3'	1	TGCAGCAAAAATTGAATTTCATAGGC CATTCAGTGTTCTCTGCGATAATT
7855	db mining	Hs.120716	AA748500		ny01h10.s1 cDNA, 3' end /clone=IMAGE:1270531 /clone_end=3'	1	CCAGGAATGGAAATACGCCAACCCA GGTTAGGCACCTCTATTGCAGAATT
7858	db mining	Hs.320428	BF512663		UI-H-BW1-amg-f-02-0-UI.s1 cDNA, 3' end /clone=IMAGE;3069842 /clone_end=3'	1	AGGAAATTGGTTGAAGTCGTTTTTCT CTTGTTAGTCTCATGTTAAGCTGT
7857	db mining	Hs.123593	AA814828	2884424	ob73d07.s1 cDNA, 3' end /clone=IMAGE:1337005 /clone_end=3'	1	TCGCCTGGGGAGAATTTAAAATCTAA GTCGCTGGAAGTCCCTTTGTATGT
7858	db mining		AA730985		nw67a04.s1 cDNA, 3' end /clone=IMAGE:1251630 /clone_end=3'	1	ACCTGTAGGAAGGGTTTGTGAATATT CTGTTGCTCTGAATTATTAGCGGT
7859	dis mining		AA811469		ob83c11.s1 cDNA, 3' end /clone=IMAGE:1337972 /clone_end=3'	1	TGAGAGGATCTTGAGACATTCTTGTG TTATTTGCCCTCTATGTTTTAGGT
7860	db mining	Hs.127156		3096266	oc10a09.s1 cDNA, 3' end /clone=IMAGE:1340440 /clone_end=3'	. 1	TCCCAAGCATGAGACAAGTACCACCA GTGGTTCAGGAGATGATTTTAGGT
7881	db mining	Hs.320486	BF513276		UI-H-BW1-amo-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070560 /clone_end=3'	1	ACAAGACAGCAGCCTTCCCGAAATGT CACTACTAAGAATTATTCAGAGGT
7862	db mining	Hs.343330	BF514718		UI-H-BW1-ans-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3083063 /clone_end=3'	1	GCTGCCCAAACTTCCATTTATTTACC CTCCAAACATCACTTCCTTC
7863	db mining	Hs.123584	AA814349		nz06h06.s1 cDNA, 3' end /clone=IMAGE:1287035 /clone_end=3'		ACATTTGCCAATGCACTTGATGTAAA GTTGTTGAGGATGTTGACTCTCCT
7864	db mining		AA811751		ob80e12.s1 cDNA, 3' end /clone=IMAGE:1337710 /clone_end=3'	1	TCCCCCTTCCTAACACCAATTTGGGA ACATCACTACTTGTATATTATCCT
7865	db mining	Hs.122860	AA766374		oa36b03.s1 cDNA, 3' end /clone=IMAGE:1307021 /clone_end=3'	1	TCAAGACCCTTAGAGTAAGTTAACTC CCAAGGAAATGTAGTTAGTTCCCT
7866	db mining	Hs.105268	AA490812	2219985	aa49e05.s1 cDNA, 3' end /done=IMAGE:824288 /done end=3'	1	AACCCACAATCCAACTCCCTTGATGA GGATGATCATTAACAACAATCACT
7867	db mining	Hs.297465	BF512677	11597856	UI-H-BW1-amg-g-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069894 /clone_end=3'	1	TTTGAAGCCTCTGGTACTTCCCCTTC CCAAACCCAGTCACAGGAAACACT
7868	db mining	Hs.127167	AA938326	3096437	oc11c08.s1 cDNA, 3' end /clone=IMAGE:1340558 /clone_end=3'	1	TTGGAGGTTAACAGTATTCCTTTGAG TGGTGTGATTAAAGGTGCTTTTAT
7869	db mining	Hs.123361	AA811359	2880970	ob82a07.s1 cDNA, 3' end /clone=IMAGE:1337844 /clone_end=3'	1	CCAACCTCCAGAACTGCCTATCTAAC TCATCTGTGGTGATGGAATGCTAT
7870	db mining	Hs.105282	AA491247	2220420	aa49b01.s1 cDNA, 3' end	1	AGTGGCTCTCTGCTGTTAGCATGGTT
7871	db mining	Hs.320385	BF512292	11597471	/clone=IMAGE:824233 /clone_end=3' UI-H-BW1-amb-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3089359 /clone_end=3'	1	ACTAATCTTTTGGTTACTTTTCAT TGACCTCAGTGTCTACTTCAGCAGAA CCTGTGGGTATATGCCTACCTCAT

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	db mining	Hs.105506			aa74c04.s1 cDNA, 3' end /clone=IMAGE:826662 /clone_end=3'	1	AAGGAGAACTGTCAACTGAATCTCAA ATGCAGTCAAATGAAGAGAGGCAT
7873	db mining	Hs.124928	AA765759	2816997	oa07h05.s1 cDNA, 3' end /clone=IMAGE:1304313 /clone_end=3'	1	TTCAAGTCATTATAGGTTTTGGGCATA CAGGGTTAACCTTGTGATGTACAT
7874	db mining	Hs.320488	BF513286	11598465	UI-H-BW1-amo-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070580	1	AGCAGAACAACATGTGTTTGACACTT TTCCTTCTCTGTAATGAGGTACAT
7875	db mining	Hs.122891	AA767801	2818816	/clone_end=3' oa45h09.s1 cDNA, 3' end /clone=IMAGE:1307969 /clone_end=3'	1	TGCCTGTGTGGGTCAAAGGAATCATC TATGCTAATGTATTTGAGCCAAAT
7876	db mining	Hs.116435	AA648285	2574714	ns20d12.s1 cDNA, 3' end /clone=IMAGE:1184183 /clone_end=3'	1	ACCGAAAGCAGCATTTTCAATGTTTA ATTAAATCGATGCAGGAAATTGTG
7877	db mining	Hs.300303	AW292760	6699396	UI-H-BW0-aij-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729453 /clone_end=3'	1	GTCCCTGGCCCTTCACTCTTCGTCCA GGCTCTCTGACCTCTTTCCCTCTG
7878	db mining	Hs.123154	AA688058	2674964	nv58c04.s1 cDNA, 3' end /clone=IMAGE:1233990 /clone_end=3'	1	TGTCCGCTGTTTTACCTCACTGCTCC TGTTTATGCCCTTAACTTCTGCTG
7879	db mining	Hs.320489	BF513296	11598475	UI-H-BW1-amo-f-11-0-ULs1 cDNA, 3' end /clone=IMAGE;3070628 /clone_end=3'	1	GCACAAGACCTCACTTGGAACAAGTA CCAGGCAGAAGAGAGCATTACCTG
7880	db mining	Hs.124353	AA830448	2903547	oc51d05.s1 cDNA, 3' end /clone=IMAGE:1353225 /clone_end=3'	1	TTTCATATCTTGGCAGTTGGATGCGG TAAGAGCCACAGAGAAACCACCTG
7881	db mining	Hs.122824	AA765319	2816557	oa01f11.s1 cDNA, 3' end /clone=IMAGE:1303725 /clone_end=3'	1	AGGACCCTTTTCCCATATTTCTGGCT ATATACAAGGATATCCAGACACTG
7882	db mining	Hs,124317	AA827178	2901175	ob53g04.s1 cDNA, 3' end /clone=IMAGE:1335126 /clone_end=3'	1	ACCAGGCCTAGAATTTAGGTTCTAGG TGTAAACTATTGGCCTATCAGATG
7883	db mining	Hs.300373	AW297820	6704445	UI-H-BW0-aiy-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731230 /clone end=3'	1	GTGCATTTTAGCAACAGACTTCCAGG TTTCCAGCGCGGGCCAGGAAGGGG
7884	db mining	Hs.320464	BF513050	11598229	UI-H-BW1-amn-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070349 /clone_end=3'	1	CTGTCATGCACCACCTCATCCCCTCC TTCAGGGCCAGGGACAGTCCCTAG
7885	db mining	Hs.313366	AW297537	6704173	UI-H-BW0-aja-f-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731160 /clone_end=3'	1	AGAGGAGGAGGGGGTAGAATGAATT TCATTTAAAGCTCAACCTAGTTCAG
7886	db ⁻ mining	Hs.320427	BF512648	11597827	UI-H-BW1-amg-d-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069762 /clone_end=3'	1	CAGTCTCCCAGCTTTCTTGGCCTCCT CTGCCAACTGGATGCAAGGCTCAG
7887	db mining	Hs.252840	AW015143	5863980	UI-H-BI0p-abb-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2711149 /clone end=3'	1	TGGAGAGAAGGTTCGGGAAGACGAG GGGGCTGGGAGGTTTGGAAAGACAG
7888	db mining	Hs.313161	AW292801	6699437	UI-H-BW0-aij-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729613 /clone_end=3'	1	CTGAAATGGGGGAAGGTGGGTTATG ACAAAGTTCATGGAGAGGCCTGAAG
7889	db mining	Hs.309124	Al380478	4190331	tf95a09.x1 cDNA, 3' end /clone=IMAGE:2107000 /clone_end=3'	1	TAAAGCGGTACGGGATTCCGCACCC TACTCCAGCAAGAAAGAGCCTGAAG
7890	db mining	Hs.120562	AA741096	2779688	ny99g07.s1 cDNA, 3' end /clone=IMAGE:1286460 /clone_end=3'	1	AGCATTCATTCCTCCAAACACACTCC CAGGGTTAGGTCTCTTACCTCTGC
7891	db mining	Hs.105530	AA521450	2261993	aa69d11.s1 cDNA, 3' end /clone=IMAGE:826197 /clone_end=3'	1	GGTGTTGAATATTTATACGGATTGGC ATCATAAGATACCGCGATACCTGC
7892	db mining	Hs.123194	AA805997	2874747	oc18g05.s1 cDNA, 3' end /clone=IMAGE:1341272 /clone_end=3'	1	ACCITAGTCTAACTGCCTTCTGTAAA GTGGGTTGCTATAGTCTTTAAGCC
7893	db mining	Hs.122833	AA765597	2816835	oa08a10.s1 cDNA, 3' end /ctone=IMAGE:1304346 /ctone_end=3'	1	TGAGGTTTGGATGGTGGCAGGTAAAA CAGAAAGGCAAGATGTCATCTGAC
7894	db mining	Hs.313827	AW452984	6993760	UI-H-BW1-amd-g-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069525 /clone_end=3'	1	TGGAGCTGCTACATAATTATTTCAGG TCTCAAAGCTTCCAAGAAGTGGAC
7895	db mining	Hs.122383	AA789140	2849260	aa66g10,s1 cDNA, 3' end	1	AGACGGAACCTGAGATGTTGGATGTT
7896	db mining	Hs.120226	AA731687	2752576	/clone=IMAGE:825954 /clone_end=3' mv58f05.s1 cDNA, 3' end /clone=IMAGE:1250817 /clone_end=3'	1	GTTGATCTTAGCAAACAGACTTTA AGATCTGTAATCTTTTGGCAAATGGAA CTCACCTGCAACGATACCTACTTA
7897	db mining	Hs.120288	AA731998	2753949	nw61b04.s1 cDNA, 3' end /clone=IMAGE:1251055 /clone_end=3'	1	GAGGACTTCCATTCCCCATTTCCCGC ATACCTGCTGTTCTGTCTGAATTA
7898	db mining	Hs.123168	AA804519	2873650	ns28a11.s1 cDNA, 3' end /clone=IMAGE:1184924 /clone_end=3'	1	AGCTCACACCTGTTCCTTCATGGGTC AGTTCCTTTCATTTTCACTTTTGA
7899	db mining	Hs.124369	AA830835	2903934	oc54b06.s1 cDNA, 3' end /clone=IMAGE:1353491 /clone_end=3'	1	AGCTGCTGCTTCTCTTTCAGTTGCAA ATGCAAACCTGTTATAATCTTTGA

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7900	db mining	Hs.122482	AA767335	2818350	nz65h02.s1 cDNA, 3' end /clone=IMAGE:1300371 /clone_end=3'	1	TCAATATCTGTGTGTCTTTTCATGAGT GGCTGTTACTTGTGAAGAATTGA
7901	db mining	Hs.313287	AW296059	6702695	UI-H-BW0-aiu-g-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730796	1	TGAGTGGACTGAGGAATGAATAGAAA ACGTGGATATATGTAGAAAGCTGA
7902	db mining	Hs.120705	AA748015	2787973	/clone_end=3' nx87c05.s1 cDNA, 3' end /clone=IMAGE:1269224 /clone_end=3'	1	ACCAGCCCCTGGGAATGTTATGAGCA AATGATACTCCATGAGTAAAATGA
7903	db mining	Hs.320495	BF513385	11598564	UI-H-BW1-amk-f-10-0-ULs1 cDNA, 3' end /clone=IMAGE:3070242	1	TCGTGTGAGTGTGAGAGACATGTTCA TTGTGAAAAGGATACTCCTAGTGGA
7904	db mining	Hs.121104	AA721020	2737155	/clone_end=3' nx89f11.s1 cDNA, 3' end /clone=IMAGE:1269453 /clone_end=3'	1	TTTGTCAAATGCCTGTTCACCATCTG TGGAAGTCATTATATGATTCAGGA
7905	db mining	Hs.124297	AA827809	2900172	od08c04.s1 cDNA, 3' end /clone=IMAGE:1367334 /clone_end=3'	1	ACACTTTTCTTCTAAGGAGAGCTTTCT TAGGCATTTCAAAGAACTTTCGA
7906	db mining	Hs.320372	BF512096	11597308	UI-H-BW1-ami-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070218 /clone_end=3'	1	ACCAAATGAGTACCATCTGTTGAACA CAGGGTGGCGATCCAAGTGTTTCA
7907	HUVEC cDNA	Hs.92381	AB007956	3413930	mRNA, chromosome 1 specific transcript KIAA0487 /cds=UNKNOWN	1	ACCTGACTTCCACGATAAAATGGAGA TGAGTGCAGGGGTGAGTGTATAGT
7908	HUVEC cDNA	Hs.24950	AB008109	2554613	regulator of G-protein signalling 5 (RGS5), mRNA /cds=(81,626)	1	TGCAGATTTATACTCCTGACGTGTCT CATTCACAGCTAAATAATAGGCCA
7909	HUVEC cDNA	Hs.306193	AB011087	3043553	hypothetical protein (LQFBS-1), mRNA	1	ACCCTCGCCCTTTCCCTCCGGTTCAG
7910	HUVEC cDNA	Hs.154919	AB014525	3327063	/cds=(0,743) mRNA for KIAA0625 protein, partial	1	TACCTATTGTTTCTCCTTTCAAAT AAGAGGAAATGGCAGAATTAAAAGCA
7911	HUVEC cDNA	Hs 153028	AB014540	3327093	cds /cds=(0,2377) mRNA for KIAA0640 protein, partial	1	GAAACAAGAAGATGGACATGGATT AAGAGTGTTTGAGTGCTTGTCATCAG
7010	HUVEC cDNA		AB014546	3327105	cds /cds=(0,1812) ring finger protein (C3HC4 type) 8	1	GTGTTTTCCTTAATAAGTAGGGAT CTGCTGTCCACTTTCCTTCAGGCTCT
					(RNF8), mRNA /cds=(112,1569)		GTGAATACTTCAACCTGCTGTGAT
7913	HUVEC cDNA		AB014576	3327165	mRNA for KIAA0676 protein, partial cds /cds=(0,3789)	1	TTCCTTGGATTCATTTCACTTGGCTA GAAATTACACTGTGCTCAATGCCT
7914	HUVEC cDNA	Hs.93675	AB022718	4204189	decidual protein induced by progesterone (DEPP), mRNA /cds=(218,856)	1	AGGTCTCTGCCACCTCCTTCTCTGTG AGCTGTCAGTCTAGGTTATTCTCT
7915	HUVEC cDNA	Hs.104305	AB023143	4589483	death effector filament-forming Ced-4- like apoptosis protein (DEFCAP), transcript variant B, mRNA /cds=(522,4811)	1	GAATAGGAGGGACATGGAACCATTTG CCTCTGGCTGTGTCACAGGGTGAG
7916	HUVEC cDNA	Hs.103329	AB023187	14133226		1	CCTGTTTAAGAAAGTGAAATGTTATG GTCTCCCCTCTTCCAATGAGCTTA
7917	HUVEC cDNA	Hs.155182	AB028959	5689408	KIAA1036 protein (KIAA1036), mRNA	1	TTTCACTTTCACACTTCATCTCATTCC
7918	HUVEC cDNA	Hs.129218	AB028997	5689484	/cds=(345,1482) DNA sequence from clone RP11- 145E8 on chromosome 10. Contains the gene KIAA1074, the 3' end of the YME11L gene for YME1 (S.cerevisiae)- like 1, ESTs, STSs, GSSs and a CpG island /cds=(166,5298)	1	TGTTGTCACTTTCCCCGAAACGA TCTGGATCAATAGCTTCCCCTCTAGG GTCTACTGATGAGTCAAATCTAAA
7919	HUVEC cDNA	Hs.8383	AB032255	6683499	bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA /cds=(366,6284)	1	TTTATCTACTGTGTGTTGTGGTGGCC TGTTGGAGGCAAATAGATCAGATT
7920	HUVEC cDNA	Hs.15165	AB037755	7243048	novel retinal pigment epithelial gene	1	GACATTTTTGTAGGATGCCTGACGAG GTGTAGCCTTTTATCTTGTTTCCG
7921	HUVEC cDNA	Hs.82113	AB049113	10257384		1	CCCAGTTTGTGGAAGCACAGGCAAG
7922	HUVEC cDNA	Hs.8180	AF000652	2795862		1	AGTGTTCTTTTCTGGTGATTCTCCA TGTTCCTTTTCCTGACTCCTCCTTGC
7923	HUVEC cDNA	Hs.147916	AF000982	2580549	polypeptide 3 (DDX3), transcript variant	1	AAACAAAATGATAGTTGACACTTT GTGACTTGTACATTCAGCAATAGCAT TTGAGCAAGTTTTATCAGCAAGCA
7924	HUVEC cDNA	Hs.75056	AF002163	2290769	mRNA /cds=(856,2844) adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA	1.	TTGCTATCGACATTCCCGTATAAAGA GAGAGACATATCACGCTGCTGTCA
7925	HUVEC cDNA	Hs,42915	AF006082	2282029	homolog (ACTR2), mRNA	1	CCTGCCAGTGTCAGAAAATCCTATTT ATGAATCCTGTCGGTATTCCTTGG
79 2 6	HUVEC cDNA	Hs.11538	AF006084	2282033	/cds=(74,1258) actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1B), mRNA /cds=(80,1198)	1	AGGGAGGGGACAGATGGGGAGCTTT TCTTACCTATTCAAGGAATACGTGC
7927	HUVEC cDNA	Hs.6895	AF006086	2282037	/cds=(80,1198) actin related protein 2/3 complex, subunit 3 (21 kD) (ARPC3), mRNA /cds=(25,561)	1	TCAAGAATTTGGGTGGGAGAAAAGAA AGTGGGTTATCAAGGGTGATTTGA
7928	HUVEC cDNA	Hs.286027	AF010313	6468761	etoposide-induced mRNA (PIG8), mRNA /cds=(72,1151)	1	TGTGATTAGGTTGTTTTCCTGTCATTT TTGAGAGACTAAAATTGTGGGGG

Table 8 7929 HUVEC cDNA Hs.79150 AF026291 2559007 chaperonin containing TCP1, subunit 4 TGGGCTTGGTCTTCCAGTTGGCATTT (delta) (CCT4), mRNA /cds=(0,1619) GCCTGAAGTTGTATTGAAACAATT 7930 HUVEC cDNA Hs 81452 AF030555 3158350 fatty-acid-Coenzyme A ligase, long-AACAAGATGAGAACAGATAAAGATTG TGTGGTGTTTTGGATTTGGAGAGA chain 4 (FACL4), transcript variant 2, mRNA /cds=(506,2641) HUVEC cDNA Hs.139851 AF035752 2665791 caveolin 2 (CAV2), mRNA TGTAGCTCCCACAAGGTAAACTTCAT TGGTAAGATTGCACTGTTCTGATT /cds=(20.508) TCACTCCCCCATTTCACTTCTTTGTCA 7932 HUVEC cDNA Hs.194709 AF037364 14030860 paraneoplastic antigen MA1 (PNMA1), mRNA /cds=(664,1725) GAGAATAGTTCTTGTTCATACTG HUVEC cDNA Hs.79516 AF039856 2773159 brain acid-soluble protein 1 (BASP1). TGGGAGTGACAAACATTCTCTCATCC 7933 mRNA /cds=(52,735) TACTTAGCCTACCTAGATTTCTCA HUVEC cDNA Hs.29417 AF039942 4730928 HCF-binding transcription factor AATGGAAGGATTAGTATGGCCTATTT Zhangfei (ZF), mRNA /cds=(457,1275) TTAAAGCTGCTTTGTTAGGTTCCT 7935 HIIVEC cDNA He 26232 6136293 mannosidase, alpha, class 2C. CCCCAGCCTAAAGCAGGGATCAGTC AF044414 member 1 (MAN2C1), mRNA TTTTCTTGTGGAATAAATCCTTGGA /cds=(56.3244) 7936 HUVEC cDNA Hs.3776 AF062072 3668065 zinc finger protein 216 (ZNF216), TGTGGTAATGCCTGTTTTCATCTGTA mRNA /cds=(288,929) AATAGTTAAGTATGTACACGAGGC 7937 HUVEC cDNA Hs.74034 AF070648 3283922 clone 24651 mRNA sequence AGATGCTTAGTCCCTCATGCAAATCA /cds=UNKNOWN ATTACTGGTCCAAAAGATTGCTGA HUVEC cDNA Hs.274230 AF074331 5052074 PAPS synthetase-2 (PAPSS2) mRNA. AAAACTGCTCTTCTGCTCTAGTACCA TGCTTAGTGCAAATGATTATTTCT complete cds /cds=(63,1907) 7939 HUVEC cDNA Hs.12540 AF081281 3415122 lysophospholipase I (LYPLA1), mRNA AGCTATTAGGATCTTCAACCCAGGTA ACAGGAATAATTCTGTGGTTTCAT (cds=(35,727) myosin IXB (MYO9B), mRNA 7940 HUVEC cDNA Hs.159629 AF092131 TCCTGCGTCTATCCATGTGGAATGCT 5138911 /cds=(0,6068) GGACAATAAAGCGAGTGCTGCCCA 7941 HUVEC cDNA Hs.273385 AF105253 7532779 guanine nucleotide binding protein (G GCCACAAAAGTTCCCTCTCACTTTCA GTAAAAATAAATAAAACAGCAGCA protein), alpha stimulating activity polypeptide 1 (GNAS1), mRNA /cds=(68,1252) 7942 HUVEC cDNA Hs.2934 AF107045 5006419 ribonucleotide reductase M1 ACTGCTTTGACTGGTGGGTCTCTAGA polypentide (RRM1), mRNA AGCAAAACTGAGTGATAACTCATG /cds=(187.2565) 7943 HUVEC cDNA Hs 158237 AF112345 6650627 Integrin alpha 10 subunit (ITGA10) GGCATTGTCTCTGTTTCCCAGTGGGG mRNA, complete cds /cds=(76,3579) TGGACAGTATATCAGATGGTCAGA 7944 HUVEC cDNA Hs.183698 AF116827 7959755 ribosomal protein L29 (RPL29), mRNA CCCTGGGCTACCATCTGCATGGGGC /cds=(29,508) TGGGGTCCTCCTGTGCTATTTGTAC 7945 HIIVEC CONA Hs 2188 AF119850 7770136 Homo sapiens, eukaryotic translation TCAAGTGAACATCTCTTGCCATCACC elongation factor 1 gamma, clone MGC:4501 IMAGE:2964623, mRNA TAGCTGCCTGCACCTGCCCTTCAG complete cds /cds=(2278,3231) 7946 HUVEC cDNA Hs 22900 AF134891 7381111 nuclear factor (erythroid-derived 2)-like TCTTGGCAGCCATCCTTTTTAAGAGT 3 (NFE2L3), mRNA /cds=(492,1694) AAGTTGGTTACTTCAAAAAGAGCA AGCTAAA GAGAGGGAACCTCATCTAA 7947 HUVEC cDNA Hs.108258 AF141968 6273777 actin cross-linking factor (ACF7). transcript variant 1, mRNA GTAACATTTGCACATGATACAGCA /cds=(51,16343) 7948 HUVEC cDNA Hs.11158 GCTGAGTGCTGGCCCTCTGCGTCTT AE151072 7106865 hypothetical protein (LOC51255), CCTTATTAACCTTGAATCCTCATTA mRNA /cds=(0,461) 7949 HUVEC cDNA Hs.179573 AF193556 6907041 collagen, type I, alpha 2 (COL1A2), TGAATGATCAGAACTGACATTTAATTC ATGTTTGTCTCGCCATGCTTCTT mRNA /cds=(139,4239) endomucin-2 (LOC51705), mRNA TCCGGGCCAAGAATTTTTATCCATGA 7050 HINEC dDNA He 41135 AF205040 8547214 AGACTITCCTACTTTTCTCGGTGT /cds=(78,863) HUVEC cDNA Hs.142908 AF219119 7158848 E2F-like protein (LOC51270), mRNA GCAGAGTTCATTGTTGCCCCTTAACA /cds=(278,979) GTTTTTCCTGAGTTTACTGAAGAA aconitase 1, soluble (ACO1), mRNA 7952 HUVEC cDNA Hs.154721 AF261088 0802307 TTATCAAGCAGAGACCTTTGTTGGGA /cds=(107,2776) GGCGGTTTGGGAGAACACATTTCT calpain 2, (m/ll) large subunit (CAPN2), 7953 HUVEC cDNA Hs.76288 AF261089 9802309 GGGTATGCTGCCTCTGTAAATTCATG mRNA /cds=(142,2244) TATTCAAAGGAAAAGACACCTTGC 7954 HUVEC cDNA Hs.152707 glioblastoma amplified sequence TTGTCTGCCCCACAATCAAGAATGTA AJ001259 2769253 TGTGTAAAGTGTGAATAAATCTCA (GBAS), mRNA /cds=(8,868) 7955 HUVEC cDNA Hs 5097 A.I002308 2959871 synaptogyrin 2 (SYNGR2), mRNA ATGCCCGGCCTGGGATGCTGTTTGG /cds=(29,703) AGACGGAATAAATGTTTTCTCATTC 7956 HUVEC cDNA Hs.143323 AJ243706 6572290 mRNA for RB-binding protein AGCAGTTTGTGATATAGCAGAGGTTT (rbbp2h1a gene) /cds=(757,5802) AAATGTACCCTCCCCTTTTATGCA Heat shock 10kD protein 1 (chaperonin TGATGCTGCCCATTCCACTGAAGTTC HUVEC cDNA Hs.1197 NM 002157 4504522 TGAAATCTTTCGTCATGTAAATAA 10) 7958 HUVEC cDNA Hs.79037 14603308 AGCAGCCTTTCTGTGGAGAGTGAGAA BC010112 Homo sapiens, heat shock 60kD protein 1 (chaperonin), clone TAATTGTGTACAAAGTAGAGAAGT MGC:19755 IMAGE:3630225, mRNA. complete cds /cds=(1705,3396) CATCTGAAGTGTGGAGCCTTACCCAT 7959 HUVEC cDNA Hs.279860 AJ400717 7573518 tumor protein, translationally-controlled

1 (TPT1), mRNA /cds=(94.612)

TTCATCACCTACAACGGAAGTAGT

					Table 8		
7980	HUVEC cDNA	Hs.165563	AK024508	10440535	DNA sequence from clone RP4- 991C20 on chromosome 20, Cortains ESTs, STSs, GSSS and CpG islands. ESTs, STSs, GSSS and CpG islands. Cortains a novel gene for a protein similar to NS28, the TPDS22 gene for two isoforms of tumor protein DS2-like protein 2, a gene for a novel Drau domain protein similar to mouse and bovine cysteine string protein with two isoforms, a per MA-1 tile gene and the 5 discorns, the CAM-1 tile gene and the so- forms, the CAM-1 tile gene and the so- mice of the control of the control of the control inport receptor similar to yeast pre- mRNA splicing factors Prp1/Zer1 and Ppp fact=0,050.	1	GCCAGGCTGGTTCCGCATGGTGATC TCCGTCTTGTATGTCTGAATGTTGG
7961	HUVEC cDNA	Hs.91146	AL050147	4884153	protein kinase D2 mRNA, complete cds /cds=(39,2675)	1	CTATTTCCAAGGCCCCTCCCTGTTTC CCCAGCAATTAAAACGGACTCATC
7962	HUVEC cDNA	Hs.66762	AL050367	4914600	mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026) /cds=UNKNOWN	1	AAAGTGCCAGAATGACTCTTCTGTGC ATTCTTCTTAAAGAGCTGCTTGGT
7963	HUVEC cDNA	Hs.165998	AL080119	5262550	PAI-1 mRNA-binding protein (PAI-	1	TTGTTGGTAGGCACATCGTGTCAAGT
7964	HUVEC cDNA	Hs.111801	AL096723	5419856	RBP1), mRNA /cds=(85,1248) mRNA; cDNA DKFZp564H2023 (from clone DKFZp564H2023) /cds=UNKNOWN	1	GAAGTAGTTTTATAGGTATGGGTT AGTCCTGTATCATCCATACTTGTACTA CCTTGTCCTATGAAGCTCTGAGA
7965	HUVEC cDNA	Hs.89434	AL110225	5817161	drebrin 1 (DBN1), mRNA /cds=(97,2046)	1	TTGGCCGCTTCCCTACCCACAGGGC CTGACTTTTACAGCTTTTCTCTTTT
7986	HUVEC cDNA	Hs.7527	AL110239	5817182	small fragment nuclease (DKFZP566E144), mRNA /cds=(77,790)	1	TATGACACAGCAGCTCCTTTGTAAGT ACCAGGTCATGTCCATCCCTTGGT
7987	HUVEC cDNA	Hs.187991	AL110269	5817043	DKFZP564A122 protein (DKFZP564A122), mRNA /cds=(2570,2908)	1	TTGGTGAGTTGCCAAAGAAGCAATAC AGCATATCTGCTTTTGCCTTCTGT
7988	HUVEC cDNA	Hs.25882	AL117665	5912262	mRNA; cDNA DKFZp586M1824 (from clone DKFZp586M1824); partial cds /cds=(0,3671)	1	TGCATAGATGACCTTTGGATTATTGG ACTCTGACTATTGGGACCCTAAAT
7969	HUVEC cDNA	Hs.17428	AL133010	6453416	RBP1-like protein (BCAA), transcript variant 2, mRNA /cds=(466,4143)	1	TGGACGCCCTAAGAAACAGAGAAAAC AGAAATAACAACCAGGAACTGCTT
7970	HUVEC cDNA	Hs.278242	AL137300	6807762	Homo sapiens, clone MGC:3214 IMAGE:3502620, mRNA, complete cds /cds=(2066,3421)	1	CAATAGCTTGTGGGTCTGTGAAGACT GCGGTGTTTGAGTTTCTCACACCC
7971	HUVEC cDNA	Hs.7378	AL137683	6807784	mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227) /cds=UNKNOWN	1	TGCACTGTACTCTCTTCATAGGATTG TAAAGGTGTTCTAATCCAATTGCA
7972	HUVEC cDNA	Hs.61289	AL157424	7018453	mRNA; cDNA DKFZp761E1512 (from clone DKFZp761E1512) /cds=UNKNOWN	1	TGAAGTCATTTCATTGGGAAGGAAAG CTGCAAAGATTATTGGGGGACTAG
7973	HUVEC cDNA	Hs.240013	AL390148	9368882	mRNA; cDNA DKFZp547A166 (from clone DKFZp547A166) /cds=UNKNOWN	1	TTTCATCTGGCCCACCCTCCTTAGAC TCTCCTCCCTTCAAGAGTTGGAGC
7974	HUVEC cDNA	Hs.22829	AW887820		602281231F1 cDNA, 5' end /clone=IMAGE:4368943 /clone_end=5'	1	GTGTAGAATTCGGATCCAGTCATCTC ACAGAACTTTCCACTAGGGTGCCA
	HUVEC cDNA		BE562833		hypothetical protein MGC14151 (MGC14151), mRNA /cds=(108,485)	1	CGGACCCCAGTTTCTTGTACCAAGGG GGAAACATGCGGGGGACCCCAATGG
	HUVEC cDNA		BE612847	9894444	clone IMAGE:3856304 5', mRNA sequence	1	TAAAGATGTCCGGGTACACTTCGCCA AGGGTTAGCGTCTTTGGGCATTTC
	HUVEC cDNA		BE876332	10325018	chromosome 9 open reading frame 5 (C9orf5), mRNA /cds=(32,2767)	1	AACACAACACTAAAACCGAACACACA CGTACTAACACACCCACGACCCAA
7978	HUVEC cDNA		BE906669	10400012	sprouty (Drosophila) homolog 4 (SPRY4), mRNA /cds=(205,525)	1	CCTTCTGGTTCTGCTTTTGACCAGCA TTTTTGTGCCCCTCTGTTACTGTG
7979	HUVEC cDNA	Hs.113029	BF025727	10733439	ribosomal protein S25 (RPS25), mRNA /cds=(63,440)	1	GATATACGAAACACACCACTGGACGA TGCGAAAAACGAGACGACATAAGC
7980	HUVEC cDNA	Hs.263339	BF107006	10889631	602377929F1 cDNA, 5' end /clone=IMAGE:4508646 /clone_end=5'	1	TGGACAGGCATGAAAGGTTACAAATG GGAGAAAACTCACACACGTTATGT
	HUVEC cDNA		BF204683		601867521F1 cDNA, 5' end /clone=IMAGE:4110052 /clone_end=5'	1	GCAGGAGAGCGAGAGAGAA GAGGCAGGAGGAGAAAGAGCGTAC
	HUVEC cDNA		BF217687	11111273	(TMSB4X), mRNA /cds=(77,211)	1	CAAGAAGCAGAAGCAGCAACCAGAG ACAGAGAGACAAACGCAGAACAACA
	HUVEC cDNA				cDNA FLJ14633 fis, clone NT2RP2000938 /cds=UNKNOWN	1	AGAGGAMAGAATAGGACCAGTGCCG AGGTATAGGGAGGAGGGCATACTAA
7984	HUVEC cDNA	Hs.293981	BF247088	11162147	Homo sapiens, clone MGC:16393 IMAGE:3939021, mRNA, complete cds /cds=(506,1900)	1	TCGGAGTAAGGGCGATTGTCTCGTTA GGTAATACATCATCTTCGTGCATA

Table 8 11250608 Homo sapiens, clone MGC:15545 AGACAAGACGAGCAACGACAACCAC 7985 HUVEC cDNA Hs.157850 BF303931 IMAGE:3050745, mRNA, complete cds AGCAGCTCCATACACTCTGCCTCTC /cds=(1045,1623) 7986 HUVEC cDNA Hs.217493 D00017 219909 annexin A2 (ANXA2), mRNA AGTGAAGTCTATGATGTGAAAGACTT TGCCTCCTGTGTACTGTGTCATAA /cds=(49,1068) mRNA for Na.K-ATPase alpha-subunit. TCACAAGACAGTCATCAGAACCAGTA 7987 HUVEC cDNA Hs.76549 D00099 complete cds /cds=(318,3389) AATATCCGTCTGCCAGTTCGATCA 7988 HUVEC cDNA Hs.330716 D10522 219893 cDNA FLJ14368 fis, clone AAACTCCTGCTTAAGGTGTTCTAATTT HEMBA1001122 /cds=UNKNOWN TCTGTGAGCACACTAAAAGCGAA mRNA for OB-cadherin-2, complete CGTGCCAGATATAACTGTCTTGTTTC 7989 HUVEC cDNA Hs.75929 D21255 575578 1 cds /cds=(476,2557) AGTGAGAGACGCCCTATTTCTATG 7990 HUVEC cDNA Hs.178710 D21260 clathrin, heavy polypeptide (Hc) TCCCTGAGGCTTGTGTATGTTGGATA (CLTC), mRNA /cds=(172,5199) TTGTGGTGTTTTAGATCACTGAGT 432358 Homo saplens, Similar to ribosomal CAGAGAAGAAACCTACTACAGAGGA 7991 HUVEC cDNA Hs.334822 D23660 protein L4, clone MGC:2966 GAAGAAGCCTGCTGCATAAACTCTT IMAGE:3139805, mRNA, complete cds /cds=(1616,2617) 7678803 hypothetical protein FLJ10326 TOAGAACATAGATATGTATTCAGCTT 7992 HUVEC cDNA Hs.262823 D28500 (FLJ10326), mRNA /cds=(2,2296) GTCTTCAAATACGGCCAAGCAGAA TTGGGGTCAAGTGAAAGGGTAGGGG 7993 HUVEC cDNA Hs.151761 D43947 603948 KIAA0100 gene product (KIAA0100), mRNA /cds=(329,6607) GATAGTCCTGATCAAGTGTGATAAA CAGCAAATCCATCTGAACTGTGGAGG 7994 HUVEC cDNA Hs.699 D50525 1167502 peptidylprolyl Isomerase B (cyclophilin B) (PPIB), mRNA /cds=(21,671) AGAAGCTCTCTTTACTGAGGGTGC CCTTCTCTTCATGTGTGTAAATCTGTA 7995 HUVEC cDNA Hs 278607 D50911 6633996 mRNA; cDNA DKFZp434N0735 (from ATATACCATTCTCTGTGGCCTGT clone DKFZp434N0735); partial cds /cds=(0,1577) 7996 HUVEC cDNA Hs.57729 D50922 1469186 Kelch-like ECH-associated protein 1 GGATGGCACTTCCCCACCGGATGGA (KIAA0132), mRNA /cds=(112,1986) CAGTTATTTTGTTGATAAGTAACCC TGAGTCAGTGTCTTTACTGAGCTGGA 7997 HUVEC cDNA Hs.240770 D59253 1060898 Homo sapiens, nuclear cap binding protein subunit 2, 20kD, clone AGCCTCTGAAAGTTATTAAAGGCA MGC:4991 IMAGE:3458927, mRNA complete cds /cds=(26,496) 7998 HUVEC cDNA Hs.155595 D63878 961447 neural precursor cell expressed, CCCACACTGCTACACTTCTGATCCCC developmentally down-regulated 5 TTTGGTTTTACTACCCAAATCTAA (NEDD5), mRNA /cds=(258,1343) GTGGCTTGCTAGTCTGTTACGTTAAC 7999 HUVEC cDNA Hs.80712 D86957 1503987 septin 2 (SEP2) mRNA, partial cds /cds=(0,1527) ATGCTTTTCTAAAATTGCTTCACG 8000 HUVEC cDNA Hs.75822 D86970 1504013 mRNA for KIAA0216 gene, complete TTGTACTCACTGGGCTGTGCTCTCCC cds /cds=(484,5229) CTGTTTACCCGATGTATGGAAATA TTTATGATTAGGTGACGAGTTGACAT 8001 HUVEC cDNA Hs.170311 D89678 3218539 heterogeneous nuclear ribonucleoprotein D-like (HNRPDL). TGAGATTGTCCTTTTCCCCTGATC transcript variant 1, mRNA /cds=(580,1842) TTGTTGTTTTCCCTGATTTAGCAAGCA 8002 HUVEC cDNA Hs.83213 J02874 178346 fatty acid binding protein 4, adipocyte (FABP4), mRNA /cds=(47,445) AGTAATTTTCTCCCAAGCTGATT TTAGAAACAAAAAGAGCTTTCCTTCT 8003 HUVEC cDNA He 177766 J03473 337423 ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) (ADPRT), CCAGGAATACTGAACATGGGAGCT mRNA /cds=(159,3203) 8004 HUVEC cDNA Hs.155560 L10284 186522 calnexin (CANX), mRNA CCATTGTTGTCAAATGCCCAGTGTCC /cds=(89,1867) ATCAGATGTGTTCCTCCATTTTCT GATGTCTGGTGCCCAATCCCAGGAA 8005 HUVEC cDNA Hs.75693 L13977 431320 prolylcarboxypeptidase (angiotensinase C) (PRCP), mRNA /cds=(29,1519) GTGAGAGCCATTTCTTTTGTACTGG 8008 HINECCONA Hs 539 1.31610 1220360 ribosomal protein S29 (RPS29), mRNA AGTTGGACTAAATGCTCTTCCTTCAG /cds=(30,200) AGGATTATCCGGGGCATCTACTCA 1 33075 536843 IQ motif containing GTPase activating TGAATTTACTTCCTCCCAAGAGTTTG 8007 HUVEC cDNA Hs.1742 protein 1 (IQGAP1), mRNA GACTGCCCGTCAGATTGTTTCTGC /cds=(467,5440) AAACACATACACACAAAACAGCAAAC 8008 HUVEC cDNA Hs.180446 L38951 893287 importin beta subunit mRNA, complete cds /cds=(337,2967) TTCAGGTAACTATTTTGGATTGCA 8009 HUVEC cDNA Hs.79572 M11233 181179 cathepsin D (lysosomal asparty) CTGAGGATGAGCTGGAAGGAGTGAG protease) (CTSD), mRNA AGGGGACAAAACCCACCTTGTTGGA /cds=(2,1240) TCTTTCTTCCCTCGTGACAGTGGTGT 8010 HUVEC cDNA Hs 273415 M11560 178350 aldolase A. fructose-hisphosphate GTGGTGTCGTCTGTGAATGCTAAG (ALDOA), mRNA /cds=(167,1261) 182113 enolase 1, (alpha) (ENO1), mRNA GCTAGATCCCCGGTGGTTTTTGTGCTC 8011 HUVEC cDNA Hs,254105 M14328 /cds=(94,1398) AAAATAAAAAGCCTCAGTGACCCA 8012 HUVEC cDNA Hs 237519 M20867 183059 vz35c09.s1 cDNA, 3' end GCATGGCTTAACCTGGTGATAAAAGC /clone=IMAGE:285040 /clone_end=3* AGTTATTAAAAGTCTACGTTTTCC 8013 HUVEC cDNA He 1239 M22324 178535 alanyl (membrane) aminopeptidase CCGCCCTGTACCCTCTTTCACCTTTC (aminopeptidase N, aminopeptidase M, CCTAAAGACCCTAAATCTGAGGAA microsomal aminopeptidase, CD13, p150) (ANPEP), mRNA /cds=(120,3023) 8014 HIVEC cDNA Hs 118126 M22960 190282 protective protein for beta-GGACAGCCCACAGGGAGGTGGTGGA galactosidase (galactosialidosis) CGGACTGTAATTGATAGATTGATTA (PPGB), mRNA /cds=(6,1448) 8015 HUVEC cDNA Hs.198281 M26252 338826 pyruvate kinase, muscle (PKM2). ATTGAAGCCGACTCTGGCCCTGGCC

CTTACTTGCTTCTCTAGCTCTCTAG

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8016	HUVEC cDNA	Hs.2050	M31166	339991	pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), mRNA	1	ACTAGACTITATGCCATGGTGCTTTC AGTITAATGCTGTGTCTCTGTCAG
8017	HUVEC cDNA	Hs.99853	M59849	182591	/cds=(67,1212) fibrillarin (FBL), mRNA /cds=(59,1024)	1	GAGCCATATGAAAGAGACCATGCCGT GGTCGTGGGAGTGTACAGGCCACC
8018	HUVEC cDNA	Hs.283473	M64098	183891	hypothetical protein PRO2900	1	ATAACAGACTCCAGCTCCTGGTCCAC
8019	HUVEC cDNA	Hs.211573	M85289	184426	(PRO2900), mRNA /cds=(271,501) heparan sulfate proteoglycan 2 (perlecan) (HSPG2), mRNA	1	CCGGCATGTCAGTCAGCACTCTGG CTGGCCTCTGTGTCCTAGAAGGGAC CCTCCTGTGGTCTTTGTCTTGATTT
8020	HUVEC cDNA	Hs.75103	M86400	189952	/cds=(40,13221) tyrosine 3-monooxygenase/hyptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA /cds=(84,821)	1	CCCAAAGCTCACTTTACAAAATATTTC CTCAGTACTTTGCAGAAAACACC
8021	HUVEC cDNA	Hs.59271	M96982	338262	U2(RNU2) small nuclear RNA auxiliary factor 1 (non-standard symbol) (U2AF1), mRNA /cds=(38,760)	1	ATGTCTGCTAGAAAGTGTTGTAGTTG ATTGACCAAACCAGTTCATAAGGG
8022	HUVEC cDNA	Hs.110802	NM_000552	9257255	von Willebrand factor (VWF), mRNA	1	CTCTGCATGTTCTGCTCTTGTGCCCT TCTGAGCCCACAATAAAGGCTGAG
8023	HUVEC cDNA	Hs.274466	NM_001403	4503472	/cds=(310,8751) eukaryotic translation elongation factor 1 alpha 1-like 14 (EEF1A1L14), mRNA	1	TGCATCGTAAAACCTTTCAGAAGGAA AGGAGAATGTTTTGTGGACACGTT
8024	HUVEC cDNA	Hs.279518	NM_001642	4502148	/cds=(620,1816) amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(72,2363)	.1	AGCCCTATTCATGTCTCTACCCACTA TGCACAGATTAAACTTCACCTACA
8025	HUVEC cDNA	Hs.76224	NM_004105	9665261	EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 1, mRNA /cds=(149,1630)	1	AGTGACAGTGAACTTAAGCAAATTAC CCTCCTACCCAATTCTATGGAATA
8026	HUVEC cDNA	Hs.19545	NM_012193	6912383	frizzled (Drosophila) homolog 4 (FZD4), mRNA /cds=(308,1919)	1	ACACATGCCCTGAATGAATTGCTAAA TTTCAAAGGAAATGGACCCTGCTT
8027	HUVEC cDNA	Hs.87125	NM_014600	7657055	EH-domain containing 3 (EHD3), mRNA /cds=(285,1892)	1	GCCACTGAACCAATCACTTTGTATGC TATGCTCCTACTGTGATGGAAAAC
8028	HUVEC CDNA	Hs.119503	NM_016091	7705432	HSPC025 (HSPC025), mRNA /cds=(33,1727)	1	AGGACCGAAGTGTTTCAAGTGGATCT CAGTAAAGGATCTTTGGAGCCAGA
8029	HUVEC cDNA	Hs,7905	NM_016224	7706705	SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA /cds=(43,1830)	1	TTCAATGGAAAATGAGGGGTTTCTCC CCACTGATATTTTACATAGAGTCA
8030	HUVEC cDNA	Hs.283722	NM_020151	9910251	GTT1 protein (GTT1), mRNA /cds=(553,1440)	1	GCTCCATGTTCTGACTTAGGGCAATT TGATTCTGCACTTGGGGTCTGTCT
8031	HUVEC cDNA	Hs.286233	NM_020414	14251213	sperm autoantigenic protein 17 (SPA17), mRNA /cds=(1210,1665)	1	GCAGCAGCTTAATTTTTCTGTATTGC AGTGTTTATAGGCTTCTTGTGTGT
8032	HUVEC cDNA	Hs.272822	S56985	298485	RuvB (E coli homolog)-like 1 (RUVBL1), mRNA /cds=(76,1446)	1	ACCTCCCACTTTGTCTGTACATACTG GCCTCTGTGATTACATAGATCAGC
8033	HUVEC cDNA	Hs.279518	S60099	300168	amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(72,2363)	1	AGCCCTATTCATGTCTCTACCCACTA TGCACAGATTAAACTTCACCTACA
8034	HUVEC cDNA	Hs.194662	S80562	1245966	calponin 3, acidic (CNN3), mRNA /cds=(83,1072)	1	ACATGGAAGACTAAACTCATGCTTAT TGCTAAATGTGGTCTTTGCCAACT
8035	HUVEC cDNA	Hs.76869	U08021	494988	nicotinamide N-methyltransferase (NNMT), mRNA /cds=(117,911)	1	AGACCCCTGTGATGCCTGTGACCTCA ATTAAAGCAATTCCTTTGACCTGT
8038	HUVEC cDNA	Hs.89657	U13991	562076	TATA box blinding protein (TBP)- associated factor, RNA polymerase II, H, 30kD (TAF2H), mRNA /cds=(17,673)	1	CGCACTACTTCACCTGAGCCACCCAA CCTAAATGTACTTATCTGTCCCCA
8037	HUVEC cDNA	Hs.1516	U20982	895253	insulin-like growth factor binding protein- 4 (IGFBP4) gene, promoter and complete	1	CTGTAGACTCAGTGCCAGCCACAGCT TCAGAGATTGTGCTCACATGGTAT
8038	HUVEC cDNA	Hs.183648	U22816	930342	protein tyrosine phosphatase, receptor type, 1 polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), mRNA /cds=(229,3837)	1	TGACAAAGGATTTTACGTTTATAAAAT TATGACAGAAGCCATGTGCCCCG
8039	HUVEC cDNA	Hs.83383	U25182	799380	thioredoxin peroxidase (antioxidant enzyme) (AOE372), mRNA /cds=(43,858)	1	GTCTGCCCTGCTGGCTGGAAACCTG GTAGTGAAACAATAATCCCAGATCC
8040	HUVEC cDNA	Hs.75888	U30255	984324	phosphogluconate dehydrogenase (PGD), mRNA /cds=(6,1457)	1	CTCGTCATACAATGCCTGATGGGCTC CTGTCACCCTCCACGTCTCCACAG
8041	HUVEC cDNA	Hs.169476	U34995	1497857	Homo sapiens, glyceraldehyde-3- phosphate dehydrogenase, clone MGC:10926 MAGE:3828129, mRNA, complete cds /cds=(2306,3313)	1	CTAGGGAGCCGCACCTTATCATGTAC CATCAATAAAGTACCCTGTGCTCA
8042	HUVEC cDNA	Hs.192023	U39067	1718194	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) (EIF3S2), mRNA /cds=(17,994)	1	TCCGTATCCATTACTTCGACCCACAG TACTTTGAATTTGAGTTTGAGGCT
8043	HUVEC cDNA	Hs.155637	U47077	13570016	DNA-dependent protein kinase catalytic subunit (DNA-PKcs) mRNA, complete cds /cds=(57,12443)	1	CCAGTCCTCCACACCCAAACTGTTTC TGATTGGCTTTTAGCTTTTTGTTG
8044	HUVEC cDNA	Hs.285313	U51869	2745959	core promoter element binding protein (COPEB), mRNA /cds=(117,968)	1	CTGTTGTCTCTCTGAGGCTGCCAGTT GTTGTGTTACCGATGCCAGAAG

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8045	HUVEC cDNA	Hs.184270	U56637	1336098	capping protein (actin filament) muscle Z-line, alpha 1 (CAPZA1), mRNA	1	AATATAGTCAAGCAAGTTTGTTCCAG GTGACCCATTGAGCTGTGTATGCA
8046	HUVEC cDNA	Hs.75064	U61234	1465773	/cds=(0,860) tubulin-specific chaperone c (TBCC), mRNA /cds=(23,1063)	1	TTTGCTATTTTCGTCATGCCTTTGAGA CTGAGTCTTACTCCGTCCCCCAG
8047	HUVEC cDNA	Hs.183684	U73824	1857236	eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA	1	TTGTGGGTGTGAAACAAATGGTGAGA ATTTGAATTGGTCCCTCCTATTAT
8048	HUVEC cDNA	Hs.165263	U89278	1877500	/cds=(306,3029) early development regulator 2 (homolog of polyhomeotic 2) (EDR2),	1	CAGGAAGGAGGTAGGCACCTTTCTG AGCTTATTCTATTC
8049	HUVEC cDNA	Hs.334703	W29012	1308969	mRNA /cds=(8,1309) Homo sapiens, clone IMAG E:3875338, mRNA, partial cds /cds=(0,930)	1	GGGAGCCATCCCTCTCTACCAAGGT GGCAATGATGGAGGGAACTTGCATG
8050	HUVEC cDNA	Hs.287820	X02761	31396	mRNA for fibronectin (FN precursor) /cds=(0,6987)	1	TGGCCCGCAATACTGTAGGAACAAG CATGATCTTGTTACTGTGATATTTT
8051	HUVEC cDNA	Hs.14376	X04098	28338	actin, gamma 1 (ACTG1), mRNA /cds=(74,1201)	1	GGTTTTCTACTGTTATGTGAGAACATT AGGCCCCAGCAACACGTCATTGT
8052	HUVEC cDNA	Hs.290070	X04412	35447	gelsolin (amyloidosis, Finnish type) (GSN), mRNA /cds=(14,2362)	1	AGCCCTGCAAAAATTCAGAGTCCTTG CAAAATTGTCTAAAATGTCAGTGT
8053	HUVEC cDNA	Hs.79086	X06323	34753	mitochondrial ribosomal protein L3 (MRPL3), mRNA /cds=(76,1122)	1	TGGGGACTATAGTGCAACCTATTTGG GTAAAGAACCATTTGCTAAAATG
8054	HUVEC dDNA	Hs.287797	X07979	31441	mRNA for FLJ00043 protein, partial cds /cds=(0,4248)	1	ACCACTGTATGTTTACTTCTCACCATT TGAGTTGCCCATCTTGTTTCACA
8055	HUVEC cDNA	Hs.87409	X14787	37464	thrombospondin 1 (THBS1), mRNA /cds=(111,3623)	1	TTGACCTCCCATTTTTACTATTTGCCA ATACCTTTTTCTAGGAATGTGCT
8056	HUVEC cDNA	Hs.82202	X53777	34198	ribosomal protein L17 (RPL17), mRNA /cds=(286,840)	1	GAGGAGGTTGCCCAGAAGAAAAAGA TATCCCAGAAGAAACTGAAGAAACA
8057	HUVEC cDNA	Hs.233936	X54304	34755	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(114,629)	1	AACCTACCAGCCCTTCTCCCCCAATA ACTGTGGGTCTATACAGAGTCAAT
8058	HUVEC cDNA	Hs.74405	X57347	32463	tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, theta polypeptide (YWHAQ), mRNA /cds=(100,837)	1	AGAGAGTTGGACCACTATTGTGTGTT GCTAATCATTGACTGTAGTCCCAA
8059	HUVEC cDNA	Hs.77813	X59960	402620	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) (SMPD1), mRNA /cds=(0,1889)	1	CCCTGTACTGCTGCTGCGACCTGATG CTGCCAGTCTGTTAAAATAAAGAT
8080	HUVEC cDNA	Hs.172690	X62535	30822	diacylglycerol kinase, alpha (80kD) (DGKA), mRNA /cds=(103,2310)	1	ACACACATACACACACCCCAAAACAC ATACATTGAAAGTGCCTCATCTGA
8061	HUVEC cDNA	Hs.272822	X83527	36127	RuvB (E coli homolog)-like 1 (RUVBL1), mRNA /cds=(76,1446)	1	ACCTCCCACTTTGTCTGTACATACTG GCCTCTGTGATTACATAGATCAGC
8082	HUVEC cDNA	Hs.119529	X87698	37476	epididymal secretory protein (19.5kD) (HE1), mRNA /cds=(10,465)	1	AACAACATTAACTTGTGGCCTCTTTCT ACACCTGGAAATTTACTCTTGAA
8063	HUVEC cDNA	Hs.211579	X68264	433891	MUC18 gene exons 1&2 /cds=(26,1966)	1	TCTCTGCTCAATCTCTGCTTGGCTCC AAGGACCTGGGATCTCCTGGTACG
8064	HUVEC cDNA	Hs.75061	X70328	38434	macrophage myristoylated alanine-rich C kinase substrate (MACMARCKS), mRNA/cds=(13,600)	1	TGTCTTACTCAAGTTCAAACCTCCAG CCTGTGAATCAACTGTGTCTCTTT
8065	HUVEC cDNA	Hs.31314	X72841	297903	retinoblastoma-binding protein 7	1	AACTTTTACACTTTTTCCTTCCAACAC
8068	HUVEC cDNA	Hs.79088	X78669	469884	(RBBP7), mRNA /cds=(287,1564) reticulocalbin 2, EF-hand calcium binding domain (RCN2), mRNA	1	TTCTTGATTGGCTTTGCAGAAAT TGGTGAGTGGAATTTGACATTGTCCA AACCTTTTTCATTTTTGAGTGATT
8067	HUVEC cDNA	Hs.7957	X79448	2326523	/cds=(66,1019) adenosine deaminase, RNA-specific (ADAR), transcript variant ADAR-a,	1	GAGTGAGGAAGACCCCCAAGCATAG ACTCGGGTACTGTGATGATGGCTGC
8068	HUVEC cDNA	Hs.76206	X79981	599833	mRNA /cds=(187,3867) cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA	1	TGGCAAAGCCCCTCACACTGCAAGG GATTGTAGATAACACTGACTTGTTT
8069	HUVEC cDNA	Hs.172182	Y00345	35569	/cds=(120,2474) poly(A)-binding protein, cytoplasmic 1	1	GGAAAGGAAACTTTGAACCTTATGTA
8070	HUVEC cDNA	Hs.180414	Y00371	32466	(PABPC1), mRNA /cds=(502,2403) hsc70 gene for 71 kd heat shock	1	CCGAGCAAATGCCAGGTCTAGCAA AGTTAAGATTATTCAGAAGGTCGGGG
8071	HUVEC cDNA	Hs.75216	Y00815	34266	cognate protein protein tyrosine phosphatase, receptor type, F (PTPRF), mRNA	1	ATTGGAGCTAAGCTGCCACCTGGT TTACCTTGTGGATGCTAGTGCTGTAG AGTTCACTGTTGTACACAGTCTGT
8072	HUVEC cDNA	Hs.65114	Y07604	1945761		1	GGGGTCTTCACATTATCATAACCTCT CCTCTAAAGGGGAGGCATTAAAAT
8073	HUVEC cDNA	Hs.113503	Y08890	2253155	/cds=(51,1343) Homo spaiens mRNA for Ran_GTP binding protein 5 (RanBP5(Importin5) gene) /cds=(236,3529)	1	TTTCCTTGTGCAATTCAGACTTAAGC ATCGAGTTTTTACCATCTTCCACT
8074	HUVEC cDNA	Hs.44499	Y09703	4581462	pinin, desmosome associated protein (PNN), mRNA /cds=(30,2261)	1	ACATGTGCAAATAAATGTGGCTTAGA CTTGTGTGACTGCTTAAGACTAAA
8075	HUVEC cDNA	Hs.8867	Y11307	2791897	cysteine-rich, anglogenic inducer, 61 (CYR61), mRNA /cds=(80,1225)	1	AAATGTAGCTTTTGGGGAGGGAGGG GAAATGTAATACTGGAATAATTTGT

					Table 8		
8076	HUVEC cDNA	Hs.90061	Y12711	6759555	progesterone receptor membrane component 1 (PGRMC1), mRNA	1	ACCCACTGCAAAAGTAGTAGTCAAGT GTCTAGGTCTTTGATATTGCTCTT
8077	HUVEC cDNA	Hs.101033	Y14391	6562622	/cds=(78,665) Pseudoautosomal GTP-binding protein- like (PGPL), mRNA /cds=(329,1540)	1	GCCTGCTGTGAACTGCTTTCCCTCGG AATGTTTCCGTAACAGGACATTAA
8078	HUVEC cDNA	Hs.24322	Y15286	2584788	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 9kD (ATP6H),	1	GAAGAGCCATCTCAACAGAATCGCAC CAAACTATACTTTCAGGATGAATT
8079	HUVEC cDNA	Hs.291904	Z31696	479156	mRNA /cds=(62,307) accessory proteins BAP31/BAP29	1	AGGAGGGTGGGTGGACAGGTGGAC
8080	HUVEC cDNA	Hs.180877	Z48950	761715	(DXS1357E), mRNA /cds=(136,876) clone PP781 unknown mRNA	1	TGGAGTTTCTCTTGAGGGCAATAAA TGCTTGATTAAGATGCCATAATAGTG
8081	HUVEC cDNA	Hs.289101	Z49835	860985	/cds=(113,523) glucose regulated protein, 58kD	1	CTGTATTTGCAGTGTGGGGCTAAGA TTGGGGGGAAATGTTGTGGGGGTGGG
8082	HUVEC cDNA	Hs.10340	AK000452	7020548	(GRP58), mRNA /cds=(0,1517) hypothetical protein FLJ20445	1	GTTGAGTTGGGGGTATTTTCTAATT AGCATGGTAAACCTGGGTTTTGTTCA
8083	HUVEC cDNA	Hs.194676	AK001313	7022490	(FLJ20445), mRNA /cds=(334,1170) tumor necrosis factor receptor superfamily, member 6b, decoy	1	TATTTTCTCCAGACAGAAATGCAA GGTCTCTTTGACTAATCACCAAAAAG CAACCAACTTAGCCAGTTTTATTT
					(TNFRSF6B), transcript variant 2, mRNA /cds=(827,4486)		CARCCARCTIAGCCAGTTTATTT
8084	HUVEC cDNA	Hs.808	AK001364	7022577	heterogeneous nuclear ribonucleoprotein F (HNRPF), mRNA /cds=(323,1570)	1	GCCCTTGATGCTGGAGTCACATCTGT TGATAGCTGGAGAACTTTAGTTTC
8085	HUVEC cDNA	Hs.15978	AK002211	7023952	cDNA FLJ11349 fis, clone PLACE4000650, weakly similar to TUBERIN /cds=UNKNOWN	1	GCCGATTCCAAGCGAGGGATTTAATC CTTACATTTTTGCCCATTTGGCTC
8086	HUVEC cDNA	Hs.29692	AK021498	10432693	cDNA FLJ11436 fis, clone HEMBA1001213 /cds=UNKNOWN	1	TTCCCTGGACAGTTTGATGTGCTTAT GGTTGAGATTTATAATCTGCTTGT
8087	HUVEC cDNA	Hs.109672	AK023900	10435975	Homo sapiens, Similar to sialytransferase 7 ((alpha-N-	1	GGCGGTGACTGCCCCAGACTTGGTT TTGTAATGATTTGTACAGGAATAAA
					salyuansierase / (alpha-4-ya- acelyineuraminyl 2,3-betagalactosyl- 1,3)-N-acelyl galactosaminide alpha-2,6- sialytransferase) F, clone MGC:14252 IMAGE:4128833, mRNA, complete cds /cds=(128,1129)		4
8088	HUVEC cDNA	Hs.25635	AK024039	10436304	cDNA FLJ13977 fis, clone Y79AA1001603, weakly similar to POLYPEPTIDE N- ACETYLGALACTOSAMINYLTRANSF ERASE (EC 2.4.1.41) /cds=(418,1791)	1	TGACCATTTGGAGGGGGGGGCCTC CTAGAAGAACCTTCTTAGACAATGG
8089	HUVEC cDNA	Hs.288967	AK024167	10436481	cDNA FLJ14105 fis, clone MAMMA1001202 /cds≖UNKNOWN	1	CAGTCCTCACACCAGCCAAGGTCACA GGCAAGAGCAAGAAGAGAAACTGA
8090	HUVEC cDNA	Hs.25001	AK024230	10436557	cDNA FLJ14168 fis, clone NT2RP2001440, highly similar to mRNA for 14-3-3gamma /cds=UNKNOWN	1	CCTCAGTGATGGAATATCATGAATGT GAGTCATTATGTAGCTGTCGTACA
8091	HUVEC cDNA	Hs.6101	AK025006	10437439	hypothetical protein MGC3178 (MGC3178), mRNA /cds=(81,1055)	1	ACACACACTTCAGCTTTGCATCACG AGTCTTGTATTCCAAGAAAATCAA
8092	HUVEC cDNA	Hs.322680	AK025200	10437684	cDNA: FLJ21547 fis, clone COL06206 /cds=UNKNOWN	1	GGAATTTCGCACCAGAGGACCCACC ACGTCCTCGCTTCGACATCTTGAAC
8093	HUVEC cDNA	Hs.288081	AK025375	10437878	actin, beta (ACTB), mRNA /cds=(73.1200)	1	GGAGGCAGCCAGGGCTTACCTGTAC ACTGACTTGAGACCAGTTGAATAAA
8094	HUVEC cDNA	Hs.288889	AK025842	10438480	nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA /cds=(342,1586)	1	CAGAGAAAGAAAAGGCAAAAGACTG GTTTGTTTGCTTAATTTCCTTCTGT
8095	HUVEC cDNA	Hs.251653	AK026594	10439481	tubulin, beta, 2 (TUBB2), mRNA /cds=(0,1337)	1	GAAAGCAGGGAAGCAGTGTGAACTC TTTATTCACTCCCAGCCTGTCCTGT
8096	HUVEC cDNA	Hs.334842	AK026632	10439528	tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(67,1422)	1	TGGTTAGATTGTTTTCACTTGGTGAT CATGTCTTTTCCATGTGTACCTGT
8097	HUVEC cDNA	Hs.288036	AK026650	10439548	tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds≕(60,1040)	1	TGCATCGTAAAACCTTCAGAAGGAAA GGAGAATGTTTTGTGGACCACTTT
8098	HUVEC cDNA	Hs.324406	AK026741	10439662	ribosomal protein L41 (RPL41), mRNA /cds=(83,160)	1	TGGACCTGTGACATTCTGGACTATTT CTGTGTTTATTTGTGGCCGAGTGT
8099	HUVEC cDNA	Hs.274368	AK026775	10439706	MSTP032 protein (MSTP032), mRNA /cds=(68,319)	1	TGCAACTAGCAACTCATCTTCGGAAG ACACAGCCAGGAGAATGAAGTAGA
8100	HUVEC cDNA	Hs.289071	AK027187	10440255	cDNA: FLJ22245 fls, clone HRC02612 /cds=UNKNOWN	1	GACTTTCCTCTCTGCGAGCTTCTACT TCTAAGTCTGAATCCAGTCAGAAA
8101	HUVEC cDNA	Hs.334788	BG385658	13278634	hypothetical protein FLJ14639 (FLJ14639), mRNA /cds=(273,689)	1	GTTTCTCTTTGGTTTTCCAGATTTTCT TTAGAACGGTGACTGACCCTCCT
8102	HUVEC cDNA	NA	NC_002090	9507429	many cloning vectors, kanamycin resistance, gene	1	CTGAGCAATAACTAGCATAACCCCTT GGGGCCTCTAAACGGGTCTTGAGG
8103	HUVEC cDNA	NA	U07360	476289	Human DXS1178 locus dinucleotide repeat polymorphism sequence	1	TGCCCATTTCACATTGCTCATTACTCA TGCAAATTTCTTCTTGCTAACCT
8104	HUVEC cDNA	Hs.230165	AA449779	2163529	zx09e02.s1 cDNA, 3' end /clone=IMAGE:785978 /clone_end=3'	1	ACCCACCATTGGTAAAATATTCAGGG GAACTTGGTTTAAAAGTTTATGCT

1915 HUVEC cDNA NA						Table 8		
1910 HUVEC cDNA Ha.172822 AMD18201 3230960 0819031 st (DNA, 3" end Chone-MAGE122399) (chone, gmd="3" AGGARAACATACCTT AGGARAACCTTACCTT CACCTACATACCTTCCTTCCCCCCTTCGCTTCACTCCCACTACACTGCTTCCCCCCCTTGCGTTGCATCCTCCCCCCTTGCGTTGCATCCTGCACACACGCCCCCCCTTGCGTGCTGCATCCTGCACACACGCCCCCCTTGCGTGCATTGCACTCCCACTACCCTACCCCTTGCGTGCATTGCACTCCCACTACCCTACCCTTACCTCTCACTCCCACTACCCTACCCTTACCTCCACTACCTCTACCTCCACTACCCTACCCTTACCCTCCCCCTTGCCTTGCATTTCCACCTCCACTACCTCTACCTCCACTACCTCCACTACCTCCACTACCTCCACTACCTCCACTACCTCCACTACCTCCACCTACCCTTACCTCCACTACCTCCACCTACCCTTACCTCCACTACCTCCACCTACCCCTCCCCCTTGCCTTGCATTTCCACTCCACTACCTCACCTCACCTCACCTTACCTCCACCTCACCTTACCTCCACCTCACCTTACCTCCACCTCACCTTACCTCCACCTCACCTTACCTCCACCTCACCTTACCTCCACCTCACCTTACCTCACCTCACCTCACCTTACCTCCACCTCACCTTACCTCACCTCACCTCACCTTACCTCACCTCACCTCACCTCACCTTACCTCACCTCACCTCACCTTACCTCACCTCACCTTACCTCACCTCACCTCACCTTACCTCACCTCACCTCACCTCACCTCACCTTACCTCACCTCACCTCACCTTACCTCACCTCACCTCACCTCACCTCACCTCACCTTACCTCACCTCACCTCACCTCACCTTACCTCACCAC	8105	HUVEC cDNA	NA	Al000459	3191013	clone IMAGE:1614158 3' similar to gb:Y00361 60S RIBOSOMAL	1	GTCAAATAAGGTTGTTCTTTCCTTGAA GGACAGCACCCATGCCACAGCAC
108 HUVEC cDNA NA A082318 341810 CX72209.x1 Source_NetNRPL_S1 CX72209.x1 Source_NRPL_S1 CX72209.x1 Source_NR	81 0 6	HUVEC cDNA	Hs.172922	AI016204	3230540	ot83f03.s1 cDNA, 3' end	1	
CCCCTTTGTTGTGTACATCCTGGC to gbtws. CCCCTTTGTTTGTTACATCTGGC to gbtws. CCCCTTTGTTTTCTT to gbtws. CCCCTTTGTTTTCTTT to gbtws. CCCCTTTGTTTTCTTTTCTTT to gbtws. CCCCTTTGTTTTTCTTTTTTTTTCTTTTTTTTTTTTT	8107	HUVEC cDNA	Hs.96457	Al081571	3418363	ox59h10.s1 cDNA, 3' end /clone=IMAGE:1660675 /clone_end=3'	1	
10	8108	HUVEC cDNA	NA	Al082318	3419110	cDNA clone IMAGE:1661870 3' similar to gb:X63527 60S RIBOSOMAL	1	
Huvec dna	8109	HUVEC cDNA	Hs.145222	Al187426	3738064	qf31d08.x1 cDNA, 3' end	1	
Second	8110	HUVEC cDNA	Hs.273194	Al285483	3923716	ty56b02.x1 cDNA, 3' end /clone=IMAGE:2283051 /clone_end=3'	1	
State	8111	HUVEC cDNA	Hs.238797	Al307808	4002412		1	
Transfer	8112	HUVEC cDNA	Hs.135872	AW028193	5886949		1	
Advance Adva	8113	HUVEC cDNA	Hs.244816	AW078847	6033999	xb18g07.x1 cDNA, 3' end /clone=IMAGE:2576700 /clone_end=3'	. 1	
	8114	HUVEC cDNA	Hs.249863	AW162315	6301348		1	
111 HUVEC cDNA NA BE672/33 10033274 767597.x NOL_CGAP_Lu24 cDNA Cone BMGE-3223169 \$ similar to TRO02231 099231 CTYDCHROME TOURS TO	8115	HUVEC cDNA	Hs.329930	AW170757	6402282	xj24e07:x1 cDNA, 3' end /clone=IMAGE:2658180 /clone_end=3'	, 1	
Company Comp	8118	HUVEC cDNA	Hs.23349	AW237511	6569900		1	
8118 HUVEC cDNA Ha.28843 BF110312 10940002 7n36086.xt cDNA 3' and / (ndon-MARGES66854.fclore_enderd*)	8117	HUVEC cDNA	NA	BE672733	10033274	clone IMAGE:3234108 3' similar to TR:O99231 O99231 CYTOCHROME	1	
A.7250 gelaltniase, 728.0 type N collagenase (MP2), mRNA A.7250 gelaltniase (MP2), mRNA A.7250 gel	8118	HUVEC cDNA	Hs.288443	BF110312	10940002	7n36d08.x1 cDNA, 3' end	1	
CCCATAGCTGCTGCGCCCATAGCTGCTGCCCCCATAGCTGCTGCCCCCATAGCTGCTGCCCCATAGCTGCTGCCCCCATAGCTGCTGCCCCCATAGCTGCTGCCCCCATAGCTGCTGCCCCCATAGCTGCTGCCCCCCCC	8119	HUVEC cDNA	Hs.111301	J03210	180670	A, 72kD gelatinase, 72kD type IV collagenase) (MMP2), mRNA	1	ACTGCCAACTCTTTGTCCGTTTTG
8121 HUVEC cDNA	8120	HUVEC cDNA	Hs.82085	M14083	189566	clade E (nexin, plasminogen activator inhibitor type 1), member 1	1	
1812 HUVEC cDNA Ha. 19349 AK000462 T020848 hypothetical protein FIL20445 (FIL20445), mRNA /cds=548,1179 T020847	8121	HUVEC cDNA	Hs.80120	Y10343	2292903	UDP-N-acetyl-alpha-D- galactosamine:polypeptide N- acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA	1	
1	8122	HUVEC cDNA	Hs.10340	AK000452	7020548	hypothetical protein FLJ20445	1	
1	8123	HUVEC cDNA	Hs.73742	AK001313	7022490	cDNA FLJ10451 fis, clone NT2RP1000959, highly similar to acidic ribosomal phosphoprotein P0 mRNA	1	CCCATCTAACTAGCACACGAACCTTC
8125 HUVEC cDNA Ha.19976 AK002211 7923982 CDNA FLJ11349 fis, clone FLACE4000058, weakly similar to TLJDERIN Index-LUNKOVNN FLACE400058, weakly similar to TLJDERIN Index-LUNKOVNN FLACE40058, weakly similar to TLJDERIN Index-LUNKOVNN TLJDERIN Index-LUNKOVNN FLACE40058, weakly similar to TLJDERIN Index-LUNKOVNN TLJDERIN INDEX-LUN	8124	HUVEC cDNA	Hs.808	AK001364	7022577	neterogeneous nuclear ribonucleoprotein F (HNRPF), mRNA	1	
1042893 CDAN FLJ11495 fls, Cone HEJB49101721 2-ds-LINNOVN 1 TTTTGGGARGAMGCTTATCCATTC HEJB49101721 2-ds-LINNOVN 1 TTTTGGGARGAMGCTTATCCATTC CTCTTTGTTGCTACTCATTC CTCTTTGTTGTACTCATTCTCCC CTCTTTGTTGCTACTCATTCTCCCC CTCTTGTTGCTACTCATTCTCCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCC CTCTTGTTGCTACTCATTCTCTCCCC CTCTTGTTGTTGCTACTCATTCTCTCCCC CTCTTGTTGTTGCTACTCATTCTCTCCCC CTCTTGTTGTTGCTACTCCATTCTCTCCCC CTCTTGTTGTTGCTACTCCATTCTCCCCCC	8125	HUVEC cDNA	Hs.15978	AK002211	7023952	cDNA FLJ11349 fis, clone PLACE4000650, weakly similar to	1	
8127 HUVEC cDNA Hs.109672 - AK023900 1043975 Homo sapiens, Similar to sightymatiserser / (lapha-h) - 1 CTCTTTGTTGCTACTCATTTCTCTCG GCGTCTGAGGGTAGGTGTC acidytheuraminyl (2.3-belaglactosy-to-sapitymatiserse) F, clone MGC;14252 HMGGE4:18283, mRNA, complete ds	8126	HUVEC cDNA	Hs.29692	AK021498	10432693	cDNA FLJ11436 fis, clone	1	
	8127	HUVEC cDNA	Hs.109672	AK023900	10435975	Homo sapiens, Similar to slatytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-slatytransferase) F, clone MGC:14252 IMAGE:4128833, mRNA, complete cds	1	CTCTTTGTTGCTACTCATTTCTCTCCG

					Table 8		
8128	HUVEC cDNA	Hs.25635	AK024039	10436304	cDNA FLJ13977 fis, clone Y79A41001603, weakly similar to POLYPEPTIDE N- ACETYLGALACTOSAMINYLTRANSF ERASE (EC 2.4.1.41) /cds=(418,1791)	1	CAACTTCCTCTTGGTTACCCAGAAGA ACAGCAGCACCGTGATCCAGAGCA
8129	HUVEC cDNA	Hs.288967	AK024167	10436481	cDNA FLJ14105 fis, clone MAMMA1001202 /cds=UNKNOWN	1	CTGTACATCTGCATCCCAGCAAAGAG CAGCAGGGACAGGAGGAGAGAG
8130	HUVEC cDNA	Hs.25001	AK024230	10436557	cDNA FLJ14168 fis, clone NT2RP2001440, highly similar to mRNA for 14-3-3gamma /cds=UNKNOWN	1	CACAGACAGAAGGTTTCGTTCCTCAT TCGACAGTGGCTCATTCAGCTCTG
8131	HUVEC cDNA	Hs.6101	AK025006	10437439	hypothetical protein MGC3178 (MGC3178), mRNA /cds≈(81,1055)	1	TCAAGATTGGCAATTCACTGTGCCCA TTAAACCACTCAGTAGCTCAGCCT
8132	HUVEC cDNA	Hs.322680	AK025200	10437664	cDNA: FLJ21547 fis, clone COL06206 /cds=UNKNOWN	1	AGTTGTCCTGAGAGTTTTACACTTGT GAGAAAATACTGGCAGCTTTGATT
8133	HUVEC cDNA	Hs.288061	AK025375		actin, beta (ACTB), mRNA /cds=(73,1200)	1	CACATAGGAATCCTTCTGACCCATGC CCACCATCACGCCCTGGTGCCTGG
8134	HUVEC cDNA	Hs.288869	AK025842	10438480	nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA /cds=(342,1586)	1	AACAGGAACCTTTATCTCTTTGTGAG GCGATTTGCATTCTCCACACAGGC
8135	HUVEC cDNA	Hs.251653	AK026594	10439481	tubulin, beta, 2 (TUBB2), mRNA /cds=(0.1337)	1	GTACTTGCCGCCGGTGGCCTCATTGT AGTACACGTTGATGCGTTCCAGCT
8136	HUVEC cDNA	Hs.278242	AK026632	10439528	Homo sapiens, clone MGC:3214 IMAGE:3502620, mRNA, complete cds /cds=(2066,3421)	1	ATAGTGGCTAGGGATTAGGAGGCGA AGGCGACAGGAGCAGACACCGGGTC
8137	HUVEC cDNA	Hs.181165	AK026650	10439548	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(53,1441)	1	CATTTTGGCTTTTAGGGGTAGTTTTC ACGACACCTGTGTTCTGGCGGCAA
8138	HUVEC cDNA	Hs.108124	AK026741	10439662	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	1	CCCTGGTTCAGGAATTAAGGGGACA GACTTGAATAAGAAACAAAACA
8139	HUVEC cDNA	Hs.274368	AK026775	10439706	MSTP032 protein (MSTP032), mRNA /cds=(68,319)	1	ACAGTAGAGAATTTGAGTACACAGGG TATGGAGAGTAGGGCACAAAATGT
8140	HUVEC cDNA	Hs.241507	AK027187	10440255	cDNA: FLJ23534 fis, clone LNG06974, highly similar to HUMRPS6A ribosomal protein S6 mRNA /cds=UNKNOWN	1	GAACAGCCTCGTCTTTCCCCGAATGC CAGGCAGGATGACGATGAACGTGG
8141	HUVEC cDNA	Hs.334788	BG392671	13286119	hypothetical protein FLJ14639 (FLJ14639), mRNA /cds≈(273,689)	1	GACCTCCAGAATTTCCTCATCGCTGT CGGTGACCAAGTCCACAGACACTA
8142	HUVEC cDNA	NA	NC_002090	9507429	many cloning vectors, kanamycin resistance, gene	1	TCTTGCCATCCTATGGAACTGCCTCG GTGAGTTTTCTCCTTCATTACAGA
8143	HUVEC cDNA	NA	U07360	476289	Human DXS1178 locus dinucleotide repeat polymorphism sequence	1	TGTTACTCCTTCAAGCCCCTGAATCA CTATAGCCACGACTCTCCAACTGA

TABLE 9: Cardiac Transplant patient RNA samples and array hybridizations

Patient #	Sample	Rejection Grade	RNA Yield (µg)	Hybridization #
	1			
14-0001	2	3A	13.6	107739
	3	1A	5.83	107740
	1			
14-0002	2			
	3			
	1	0	12.8	
14-0003	2			
	3			
14.0004	1			
14-0004	2			
	1	3A	1.08	107741
14.0005	2	0	11.2	107742
14-0005	3			
	4			
	1	2	2.02	
14-0006	2			
	3			

 $\ensuremath{\mathsf{TABLE}}\xspace\,10\text{:}\,$ Differentially expressed probes between samples from patients with high and low grade rejection:

Oligo#	Gene Represented
7401	cDNA clone IMAGE:915561
1796	amphiregulin
4423	partial IGVH3 gene for immunoglobulin heavy chain V region
4429	partial IGVL1 gene for immunoglobulin lambda light chain V region
4430	partial IGVH3 DP29 gene for immunoglobulin heavy chain V region
4767	cDNA clone COL09252, highly similar to CD24
4829	oncostatin M
8091	mRNA for a predicted protein

We claim:

A system for detecting gene expression comprising at least two isolated DNA
molecules wherein each isolated DNA molecule detects expression of a gene wherein
said gene is selected from the group of genes corresponding to the oligonucleotides
depicted in SEQ ID NO:1 - SEQ ID NO: 8143.

- 2. The system of claim 1 wherein said gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO: 2476, SEQ ID NO: 2407, SEQ ID NO: 2192, SEQ ID NO: 2283, SEQ ID NO:6025, SEQ ID NO: 4481, SEQ ID NO:3761, SEQ ID NO: 3791, SEQ ID NO:4476, SEQ ID NO: 4398, SEQ ID NO:7401, SEQ ID NO: 1796, SEQ ID NO:4423, SEQ ID NO: 4429, SEQ ID NO:4430, SEQ ID NO: 4767, SEO ID NO:4829, and SEO ID NO: 8091.
- The system of claim 1 wherein the DNA molecules are synthetic DNA, genomic DNA. PNA or cDNA.
- The system of claim 1 wherein the isolated DNA molecules are immobilized on an array.
- 5. The system of claim 4 wherein the array is selected from the group consisting of a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, polynucleotide array or a cDNA array, a microtiter plate, a membrane and a chip.
- A method of detecting gene expression comprising a) isolating RNA and b) hybridizing said RNA to the isolated DNA molecules of claim 1.
- A method of detecting gene expression comprising a) isolating RNA; b)
 converting said RNA to nucleic acid derived from the RNA and c) hybridizing said
 nucleic acid derived from the RNA to the isolated DNA molecules of claim 1.
- The method of claim 7 wherein said nucleic acid derived from the RNA is cDNA.

A method of detecting gene expression comprising a) isolating RNA; b)
converting said RNA to cRNA or aRNA and c) hybridizing said cRNA or aRNA to
the isolated DNA molecules of claim 1.

- 10. A candidate library comprising at least two isolated oligonucleotides wherein the oligonucleotides have nucleotide sequences having at least 40-50, 50-60, 70-80, 80-85, 85-90, 90-95 or 95-100% sequence identity to the nucleotide sequences selected from the group consisisting of SEQ ID NO:1- SEQ ID NO: 8143.
- 11. The candidate library of claim 10, wherein the nucleotide sequence comprises deoxyribonucleic acid (DNA) sequence, ribonucleic acid (RNA) sequence, synthetic oligonucleotide sequence, protein nucleic acid (PNA) sequence or genomic DNA sequence.
- The candidate library of claim 11, wherein the candidate library is immobilized on an array.
- 13. The candidate library of claim 12, wherein the array is selected from the group consisting of: a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, polynucleotide array or a cDNA array, a microtiter plate, a membrane and a chip.
- 14. A diagnostic oligonucleotide for a disease comprising an oligonucleotide wherein the oligonucleotide has a nucleotide sequence selected from the group consisting of SEQ ID NO:1 SEQ ID NO: 8143 wherein said oligonucleotide detects expression of a gene that is differentially expressed in leukocytes in an individual with at least one disease criterion for at least one leukocyte-related disease compared to the expression of said gene in an individual without the at least one disease criterion, wherein expression of the gene is correlated with the at least one disease criterion.
- The diagnostic oligonucleotide of claim 14, wherein the nucleotide sequence comprises DNA, cDNA, PNA, genomic DNA, or synthetic oligonucleotides.

16. The diagnostic oligonucleotide of claim 14, wherein the disease criterion comprises data wherein the data is selected from physical examination data, laboratory data, patient historic, diagnostic, prognostic, risk prediction, therapeutic progress, and therapeutic outcome data.

- 17. The diagnostic oligonucleotide of claim 14, wherein the leukocytes comprise peripheral blood leukocytes or leukocytes derived from a non-blood fluid.
- 18. The diagnostic oligonucleotide of claim 17, wherein the non-blood fluid is isolated from the colon, sinus, esophagus, small bowel, pancreatic duct, biliary tree, ureter, vagina, cervix uterus, nose, ear, urethra, eye, open wound, abscess, stomach, cerebral spinal fluid, peritoneal fluid, pleural fluid, synovial fluid, bone marrow and pulmonary lavage.
- 19. The diagnostic oligonucleotide of claim 14, wherein the leukocytes comprise leukocytes derived from urine or a biopsy sample.
- The diagnostic oligonucleotide of claim 14, wherein the leukocytes are peripheral blood mononuclear cells or T-lymphocytes.
- 21. The diagnostic oligonucleotide of claim 14, wherein the disease is selected from the group consisting of cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosis (SLE), rheumatoid arthritis, osteoarthritis, and cytomegalovirus infection.
- 22. The diagnostic oligonucleotide of claim 14, wherein the differential expression is one or more of: a relative increase in expression, presence of expression or absence of expression.
- 23. A diagnostic agent comprising an oligonucleotide wherein the oligonucleotide has a nucleotide sequence selected from the group consisting of SEQ ID NO:1 SEQ ID NO: 8143 wherein said oligonucleotide detects expression of a gene that is differentially expressed in leukocytes in an individual over time.

24. The agent of claim 23 wherein said oligonucleotide is selected from the group consisting of SEQ ID NO:2476, SEQ ID NO: 2407, SEQ ID NO:2192, SEQ ID NO:2283, SEQ ID NO:6025, SEQ ID NO:4481, SEQ ID NO:3761, SEQ ID NO:3791, SEQ ID NO:4476, SEQ ID NO:4398, SEQ ID NO:7401, SEQ ID NO:1796, SEQ ID NO:4423, SEQ ID NO:4429, SEQ ID NO:4430, SEQ ID NO:4767, SEO ID NO:4829, and SEO ID NO:8091.

- 25. A diagnostic probe set for a disease comprising at least two probes wherein each probe detects expression of a gene wherein the gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO: 1 SEQ ID NO:8143 wherein each gene is differentially expressed in leukocytes in an individual with at least one disease criterion for a disease selected from Table 1 as compared to the expression of the gene in leukocytes in an individual without the at least one disease criterion, wherein expression of the gene is correlated with the at least one disease criterion.
- An isolated nucleic acid wherein said nucleic acid comprises a sequence depicted in SEQ ID NO:8144 - SEQ ID NO:8766.
- 27. An expression vector containing the nucleic acid of claim 26 in operative association with a regulatory element which controls expression of the nucleic acid in a host cell.
- 28. A host cell comprising the expression vector of claim 27.
- The host cell of claim 27, wherein the host cell is a prokaryotic cell or a eukaryotic cell.
- 30. A kit comprising the system of claim 1.
- 31. A system for detecting gene expression in leukocytes comprising an isolated DNA molecule wherein said isolated DNA molecule detects expression of a gene wherein said gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO: 1-SEQ ID NO: 8143 and said gene is differentially expressed in said leukocytes in an individual with at least one disease

criterion for a disease selected from Table 1 compared to the expression of said gene in leukocytes in an individual without the at least one disease criterion.

- 32. The system of claim 31 wherein the DNA molecule is at least 16 nucleotides in length.
- The system of claim 31 wherein the DNA molecules are synthetic DNA, genomic DNA, PNA or cDNA.
- 34. The system of claim 31 wherein the isolated DNA molecule is immobilized on an array.
- 35. The system of claim 34 wherein the array is selected from the group consisting of a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, polynucleotide array or a cDNA array, a microtiter plate, a membrane and a chip.
- 36. A method of detecting gene expression comprising a) isolating RNA and b) hybridizing said RNA to the isolated DNA molecule of claim 31.
- 37. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to nucleic acid derived from the RNA and c) hybridizing said nucleic acid derived from said RNA to the isolated DNA molecules of claim 31.
- The method of claim 37 wherein said nucleic acid derived from the RNA is cDNA.
- 39. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to cRNA or aRNA and c) hybridizing said cRNA or aRNA to the isolated DNA molecule of claim 31.
- 40. A method of diagnosing a disease comprising obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31 and comparing the expression of the gene with a molecular signature indicative of the presence or absence of said disease.

41. A method of monitoring progression of a disease comprising: obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of disease progression.

- 42. A method of monitoring the rate of progression of a disease comprising: obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of disease progression.
- 43. A method of predicting therapeutic outcome comprising: obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the predicted therapeutic outcome.
- 44. A method of determining prognosis for a patient comprising obtaining a leukocyte sample from a patient, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene, and comparing the expression of the gene with a molecular signature indicative of the prognosis.
- 45. A method of predicting disease complications in an individual comprising obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of disease complications.
- 46. A method of monitoring response to treatment in an individual, comprising obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of response to treatment.

47. The method according to claim 46, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.

- 48. The method according to claim 41, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.
- 49. The method according to claim 42, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.
- 50. The method according to claim 43, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.
- 51. The method according to claim 44, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.
- 52. The method of claim 50, wherein the genotype is analyzed by one or more methods selected from the group consisting of Southern analysis, RFLP analysis, PCR, single stranded conformation polymorphism, and SNP analysis.
- 53. A method of RNA preparation suitable for diagnostic expression profiling comprising: obtaining a leukocyte sample from a subject, adding actinomycin-D to a final concentration of 1 ug/ml, adding cycloheximide to a final concentration of 10 ug/ml, and extracting RNA from the leukocyte sample.
- 54. The method of claim 52, wherein the actinomycin-D and cycloheximide are present in a sample tube to which the leukocyte sample is added.

Figure 1: Novel Gene Sequence Analysis

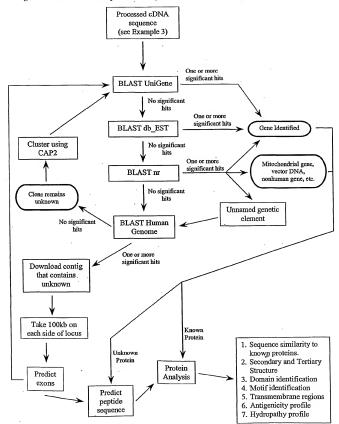
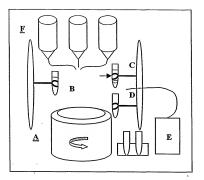


Figure 2. Automated Mononuclear Cell RNA Isolation Device



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Figure 3: Kits for discovery of, or application of diagnostic gene sets

A. Contents of kit for discovery of diagnostic gene sets

- 1. Sterile, endotoxin and RNAse free blood collection tubes (>10cc capacity)
- 2. Alcohol swabs, tourniquet, 18g needle and syringe (>10cc capacity)
- 3. Erythrocyte lysis buffer
- 4. Leukocyte lysis buffer
- 5. Substrates for labeling of RNA (may vary for various expression profiling techniques)

For fluorescence cDNA microarray expression profiling:

Reverse transcriptase and 10x RT buffer

Poly-dT primer

DTT

Deoxynucleotides 100mM each

RNAse inhibitor

Cy3 and Cy5 labeled deoxynucleotides

- 6, cDNA microarrays containing candidate gene libraries
- 7. Cover slips for slides
- 8. hybridization chambers
- 9. Software package for identification of diagnostic gene set from data

Contains statistical methods.

Allows alteration in desired sensitivity and specificity of gene set.

Software facilitates access to and data analysis by centrally located database server.

- Password and account number to access central database server.
- 11. Kit User Manual

B. Contents of kit for application of diagnostic gene sets

- 1. Sterile, endotoxin and RNAse free blood collection tubes (>10cc capacity)
- 2. Alcohol swabs, tourniquet, 18g needle and syringe (>10cc capacity)
- 3. Erythrocyte lysis buffer
- 4. Leukocyte lysis buffer
- 5. Substrates for labeling of RNA (may vary for various expression profiling techniques)

For fluorescence cDNA microarray expression profiling:

Reverse transcriptase and 10x RT buffer

Poly-dT primer

DTT

Deoxynucleotides 100mM each

RNAse inhibitor

Cv3 and Cv5 labeled deoxynucleotides

- 6. cDNA microarrays containing diagnostic gene sets
- 7. cover slips for slides
- 8. hybridization chambers
- 9. Software package for identification of diagnostic gene set from data

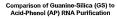
Contains statistical methods.

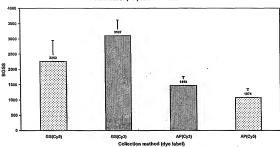
Allows alteration in desired sensitivity and specificity of gene set.

Software facilitates access to and data analysis by centrally located database

- Password and account number to access central database server.
- 11. Kit User Manual

Figure 4





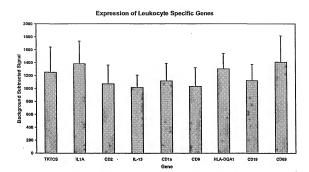
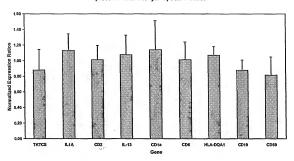
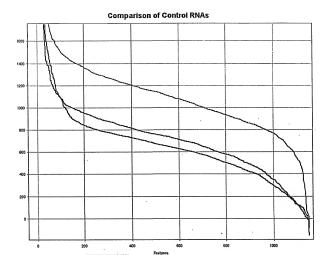


Figure 5

Figure 6







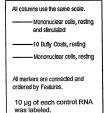


Figure 7

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Figure 8: Log expression of each probe using the R50 reference RNA. Probe expression is ordered by Signal to noise, S/N, decreasing from left to right.

Array Hybe 115018

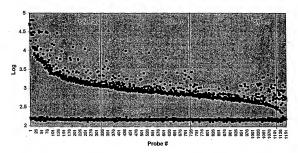


Figure 9

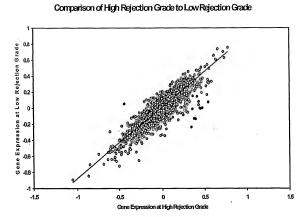


Figure 10: Differential gene expression between grade 0 and 3A samples:

	Probe		Array	107742	: Grade	e 0	Array	107739	Grad	e 3A	Ratio of	SRs
Acc#	Name	Olloo ID	F633 Median - B633	F532 Median - B532	Cy3/Cy5	SR: scaled	F833 Median - B623	F532 Medlan - B532		SR: scaled		
NM 003202					Ratio	ratio (q!r)			Ratio			Grade 3A/0
BE220969	transcription factor 7 (T-cell specific, HMG-box) (TCF7), major histocompatibility complex, class II, DQ beta 1 (HI	2476 L 6025	5558						0.051438		3.23048873	
8E220959	major histocompalibility complex, class ii, DQ beta 1 (Ht	L 6025	1810			1,318579			0.117209		3.14462275	
NM 002922	regulator of G-protein signalling 1 (RGS1), mRNA Ads=		1402			1.305545	1884	247 75	0.116455		3.13371968	
NM 001781	CD59 antigen (p60, early T-cell activation antigen) (CD5					0.369371	7385				3.11833431	0.32088403
NM 002341	hymphotoxin beta (TNF superfamily, member 3) (LTB), tr	2192				0.960516			0.034394		3,00195843	
BE220959									0.091258		2,94207495	
NM 001781	major histocompatibility complex, class II, DQ beta 1 (HI					1,257707	1942			0,436591		
U05040	CD69 anligen (p60, early T-cell activation antigen) (CD6					0.376823			0.0366			
X14008	for upstream element (FUSE) binding protein 1 (FUBP1	3581							0.09205			
	nuclear receptor subfamily 4, group A, member 2 (NR4A					0,459827			0.045488		2.82568318	
NM_003202	transcription factor 7 (T-cell specific, HMG-box) (TCF7),	2476				0.672539			0.067043			
AF035947	cytokine-inducible inhibitor of signalling type 1b mRNA,	642				2.004771			0.203302			
NM_001781	CD69 antigen (p60, early T-cell activation antigen) (CD6	2192	3357	356	0.106047	0.398574	5953	246	0.041254	0.147585	2,70062225	0.37028503
1000			11				100					
Y14737	mRNA for immunoglobulin lambda heavy chain /cds=(65				0.178417	0.670576		5787		3.144527	0.21325167	
Y14737	mRNA for immunoglobulin lembda heavy chain /cds=(6)	5 4905		240	0.171674	0,645231	7159	6112	0.853751	3.054262	0.21125570	4.73359863
BC005402	mRNA for immunoclobulin lambda heavy chain /cds+(6)	5 4481	1826	295	0.181555	0.6072	2973	2498	0.840225	3,005889	0.20200364	4.95040579
X57812	rearranged immunoclobulin lambda light chain mRNA /c	3761	6512	747	0,114711	0.431139	27381	17730	0.647529	2,316513	0.18811538	5.37301111
X57812	rearranged immunoglobulin tambda light chain mRNA /c	3761	6728	755	0.112218	0.42176	28820	18636	0.646634	2.313311	0.18232143	5,48481867
X72475	cDNA; FLJ21321 fis, clone COL02335, highly similar to	3790	8572	1188	0,138591	0.520889	17322	13892	0.801986	2,860076	0.18155283	
X72475	cDNA: FLJ21321 fis. clone COL02335, highly similar to	3790	15538	2126					0.807877			
X72475	cDNA; FLJ21321 fis, clone COL02335, highly similar to	3791	11974	1550	0.130115	0.40903	24281	10701	0.773299	2.700445	0.17877319	
X57812	rearranged immunoglobulin ismbda light chain mRNA A									2,403886		
X72475	cONA; FLJ21321 fis, clone COL02335, highly similar to	379								2.924735		
X72475	cONA: FLJ21321 fis, clone COL02335, highly similar to					0.485			0.811936			
AF067420	SNC73 protein (SNC73) mRNA, complete cds /cds=139								0.57599			
X72476	cDNA: FLJ21321 fis, clone COL02335, highly similar to								0.656601			
AF067420	SNC73 protein (SNC73) mRNA, complete cds /cds=r39											
AF067420	SNC73 protein (SNC73) mRNA, complete cds /cds=(38					0.31539				2.170163		
BC002963	rearranged immunoglobulin mRNA for mu heavy chain	e 447				0.34104			0.668500			
8C002963	rearranged immunoclobulin mRNA for mu heavy chain					0.33844						
BC002963	rearranged immunoclobulin mRNA for mu heavy chain					0.33613						
8C002963	rearranced immunoclobulin mRNA for mu heavy chain											
BC002963	rearranged immunoglobulin mRNA for mu heavy chain					0.34582						
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governing a warrend and a second contraction of the second contraction
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gc 24:
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1263/1427

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tcccattggg ggaaattttt cttttgggtta aattatttta at	ttatgggaa tgaaaactta 180
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	ggataca	atct	actgaagaca	ttcaagaaga	aaaagataaa	aaagggagtg	attgtagttc	240
	cttgtca	agag	agtgagagta	cctcggggga	agaagcatgc	atgtctgtgc	tgatcccagt	300
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						ttttgtcgaa		360
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atgaataatt cccaagggga tggtgaacat tttgcacacc caccctcaga agttaaaatg
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Gln His Phe Phe Glu Tyr Leu Leu Val Val Ser Leu Lys Lys Lys Arg 65 70 75 80

Ser Glu Asp Asp Tyr Glu Pro Ile Ile Thr Tyr Gln Phe Pro Lys Arg 85 90 95

Glu Asn Leu Leu Arg Gly Gln Gln Glu Glu Glu Glu Arg Leu Lys 100 105 110

Ala Ile Pro Leu Phe Cys Phe Pro Asp Gly Asn Glu Trp Ala Ser Leu 115 120 125

Thr Glu Tyr Pro Ser Leu Ser Cys Lys Thr Pro Gly Leu Leu Ala Ala 130 135 140

Leu Val Val Glu Lys Ala Gln Pro Arg Thr Cys Cys His Ala Ser Ala 145 150 155 160

Pro Ser Ala Ala Pro Gln Ala Arg Gly Pro Asp Ala Pro Ser Pro Ala 165 170 175

Ala Gly Gln Ala Leu Pro Ala Gly Pro Gly Pro Arg Leu Pro Lys Val 180 185 190

Tyr Cys Ile Ile Ser Cys Ile Gly Cys Phe Gly Leu Phe Ser Lys Ile 195 200 205

Leu Asp Glu Val Glu Lys Arg His Gln Ile Ser Met Ala Val Ile Tyr Pro Phe Met Gln Gly Leu Arg Glu Ala Ala Phe Pro Ala Pro Gly Lys Thr Val Thr Leu Lys Ser Phe Ile Pro Asp Ser Gly Thr Glu Phe Ile Ser Leu Thr Arg Pro Leu Asp Ser His Leu Glu His Val Asp Phe Ser Ser Leu Leu His Cys Leu Ser Phe Glu Gln Ile Leu Gln Ile Phe Ala Ser Ala Val Leu Glu Arg Lys Ile Ile Phe Leu Ala Glu Gly Leu Arg Glu Glu Glu Lys Asp Val Arg Asp Ser Thr Glu Val Arg Gly Ala Gly Glu Cys His Gly Phe Gln Arg Lys Gly Asn Leu Gly Lys Gln Trp Gly Leu Cys Val Glu Asp Ser Val Lys Met Gly Asp Asn Gln Arg Gly Thr Ser Cys Ser Thr Leu Ser Gln Cys Ile His Ala Ala Ala Ala Leu Leu Tyr Pro Phe Ser Trp Ala His Thr Tyr Ile Pro Val Val Pro Glu Ser Leu Leu Ala Thr Val Cys Cys Pro Thr Pro Phe Met Val Gly Val Gln Met Arg Phe Gln Glu Val Met Asp Ser Pro Met Glu Glu Ile Gln Pro Gln Ala Glu Ile Lys Thr Val Asn Pro Leu Gly Val Tyr Glu Glu 

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Arg Gly Pro Glu Lys Ala Ser Leu Cys Leu Phe Gln Val Leu Leu Val

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